

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 25, 2003, 10:35:03 ; Search time 85 Seconds  
(without alignments)  
1251.139 Million cell updates/sec

Title: US-10-057-609B-3

Perfect score: 3448

Sequence: 1 MAAATTTTSSISFETKP.....IPNGCTNDVITGEGRIKY 670

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_19Jun03.\*

- 1: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.\*
- 2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.\*
- 3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.\*
- 4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.\*
- 5: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.\*
- 6: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.\*
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- 8: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT.\*
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- 10: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT.\*
- 11: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT.\*
- 12: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT.\*
- 13: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT.\*
- 14: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT.\*
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- 18: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.\*
- 19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.\*
- 20: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT.\*
- 21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.\*
- 22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.\*
- 23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.\*
- 24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3448	100.0	670	19 AAW59147	A. thaliana acetol
2	3448	100.0	670	22 AAE02400	Arabidopsis thalia
3	3443	99.9	670	18 AAW22457	Arabidopsis wild-t
4	3443	99.9	670	19 AAW59146	A. thaliana acetol
5	3443	99.9	670	21 AAG54287	Arabidopsis thalia
6	3442	99.8	670	23 AAO15640	Modified Arabidops
7	3435	99.6	670	12 AAR11975	Tobacco herbicide-
8	3435	99.6	670	13 AAR26913	ALS mutant of Arap
9	3435	99.6	670	16 AAR63082	Herbicide-resistan

10	3435	99.6	670	18 AAW22464	Arabidopsis herbic
11	3425.5	98.3	669	13 AAR24800	Ser653 deleted ace
12	3422.5	98.3	669	13 AAR28618	Ala122 deleted ace
13	3422.5	98.3	669	13 AAR28619	Ala205 deleted ace
14	3422.5	98.3	669	13 AAR28623	Val171 deleted ace
15	3421.5	99.2	669	13 AAR28620	Iys256 deleted ace
16	3421.5	99.2	669	13 AAR28621	Met351 deleted ace
17	3420.5	99.2	669	13 AAR28617	Gly121 deleted ace
18	3420.5	99.2	669	13 AAR28622	Asp376 deleted ace
19	3420.5	99.2	669	13 AAR28624	Phe578 deleted ace
20	3419.5	98.2	669	13 AAR24799	Pro197 deleted ace
21	3412.5	99.0	669	13 AAR24798	Trp574 deleted ace
22	3408	98.8	666	13 AAR28616	Amino acids 650-65
23	3408	98.8	668	13 AAR24801	Pro197/Ser653 dele
24	3407.5	98.8	667	13 AAR28612	Amino acids 255-25
25	3403	98.7	666	13 AAR28610	Amino acids 194-19
26	3402	98.7	666	13 AAR28609	Amino acids 119-12
27	3396.5	98.5	665	13 AAR28614	Amino acids 373-37
28	3390	98.3	664	13 AAR28613	Amino acids 348-35
29	3382	98.1	662	13 AAR28611	Amino acids 201-20
30	3364	97.6	660	13 AAR28615	Amino acids 569-57
31	2834	82.2	547	21 AAG54288	Arabidopsis thalia
32	2763.5	80.1	557	9 AAP81151	Herbicide resistan
33	2685	77.9	666	19 AAW79141	Plant acetolactate
34	2685	77.9	666	23 ABB08419	N. plumbaginifolia
35	2683	77.8	664	18 AAW22455	Tobacco wild-type
36	2671	77.5	648	18 AAW24473	Herbicide-sensitiv
37	2664.5	77.3	667	18 AAW22456	Tobacco wild-type
38	2662	77.2	664	17 AAW00211	Tobacco Hra mutant
39	2658.5	77.1	667	12 AAR11974	Tobacco SURA-C3 mu
40	2658.5	77.1	667	13 AAR26912	ALS C3 mutant of t
41	2658.5	77.1	667	16 AAR63081	ALS SURA-C3 (P197E
42	2658.5	77.1	667	17 AAW00212	Tobacco C3 mutant
43	2658.5	77.1	667	18 AAW22462	Tobacco C3 herbici
44	2658	77.1	664	9 AAP81149	Herbicide resistan
45	2657	77.1	667	9 AAP81150	Herbicide resistan

ALIGNMENTS

RESULT 1				
AAW59147				
ID	AAW59147 standard; Protein; 670 AA.			
XX				
AC	AAW59147;			
XX				
DT	13-AUG-1998 (first entry)			
XX				
DE	A. thaliana acetolactate synthase S653N mutant.			
XX				
KW	Acetolactate synthase; ALS; imidazolinone resistance; herbicide; crop;			
KW	mutant; biosynthesis; valine; leucine; isoleucine; weed removal.			
XX				
OS	Arabidopsis thaliana.			
OS	Synthetic.			
XX				
FH	Key			
FT	Modified-site			
FT	653			
FT	/label= S653N			
XX				
XX	/note= "Wild type Ser is replaced by Asn"			
PN	US5767366-A.			
XX				
PD	16-JUN-1998.			
XX				
PF	22-DEC-1994; 94US-0363208.			
XX				
PR	19-FEB-1991; 91US-0657429.			
PR	15-DEC-1992; 92US-0990416.			
XX				
XX	22-DEC-1994; 94US-0363208.			
XX				
PA	(LOU ) UNIV LOUISIANA STATE.			

XX PI Murai N, Sathasivan K;  
 XX WPI; 1998-361818/31.  
 XX N-PSDB; AAV11891.  
 XX Imidazolinone resistant mutant acetolactate synthase gene - useful  
 PT for transforming plants and plant cells to confer resistance to the  
 FT herbicide  
 XX PS Claim 9; Fig 1A-B; 20pp; English.  
 XX This sequence represents a mutant Arabidopsis thaliana acetolactate  
 CC synthase (ALS) protein which is a key enzyme in the biosynthesis of  
 CC valine, leucine and isoleucine in plants. The wild type form of the  
 CC enzyme is inhibited by herbicides containing imidazolinone e.g.  
 CC imazapyr, imazaquin and imazepathyr. This mutant form of this ALS,  
 CC carrying a mutation where a wild type Ser residue is replaced by an  
 CC Asn at position 653 of the translated protein, results in an  
 CC imidazolinone resistant ALS. Transformed plants and cells can be used  
 CC to confer imidazolinone resistance on crops, so the herbicide can  
 CC be used in the removal of weeds. Current genetic engineering techniques  
 CC allow the transfer of the gene to different plant species. Traditional  
 CC imidazolinone resistance was only possible by classical breeding  
 CC techniques, which did not allow trait transfer out of a maize line.  
 XX SQ Sequence 670 AA;  
 Query Match 100.0%; Score 3448; DB 19; Length 670;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-278;  
 Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAATTTTSSSISSTKPSKSKPLPSRSLPSLNPKNSSSSRRGIGKSSPS 60  
 DB 1 MAATTTTSSSISSTKPSKSKPLPSRSLPSLNPKNSSSSRRGIGKSSPS 60  
 QY 61 SISAVLNTTNTTSPSTPKTKPTETISRFAPDPKRGADILVEALERQGVETVFAFG 120  
 DB 61 SISAVLNTTNTTSPSTPKTKPTETISRFAPDPKRGADILVEALERQGVETVFAFG 120  
 QY 121 GASMEIHALTRSSSRNVLPHEGGVFAAGYARSSCKGICGATSGCATNLVSLA 180  
 DB 121 GASMEIHALTRSSSRNVLPHEGGVFAAGYARSSCKGICGATSGCATNLVSLA 180  
 QY 181 DALLDSVPLVAITGVQPRRMIGTDAFQETPIVEVTSITKKNYLMVDVEDIPRIIEAFF 240  
 DB 181 DALLDSVPLVAITGVQPRRMIGTDAFQETPIVEVTSITKKNYLMVDVEDIPRIIEAFF 240  
 QY 241 LATSGRPGVPLVDVKDIOQQLAIPNWEQAMRLPGYMSMPKPPEDSHLEQIVRLISSSK 300  
 DB 241 LATSGRPGVPLVDVKDIOQQLAIPNWEQAMRLPGYMSMPKPPEDSHLEQIVRLISSSK 300  
 QY 301 KPVLVGGGCLNSDELGRFVBLTGIPVASTLMGLGSVPCDDLSLHMLGMGTYYANYA 360  
 DB 301 KPVLVGGGCLNSDELGRFVBLTGIPVASTLMGLGSVPCDDLSLHMLGMGTYYANYA 360  
 QY 361 VEHSDLLIARFPDRVTKLEAPASAKIVHIDDSAEIGKNTKTHSVGCDVKLALQ 420  
 DB 361 VEHSDLLIARFPDRVTKLEAPASAKIVHIDDSAEIGKNTKTHSVGCDVKLALQ 420  
 QY 421 GNKKVLENRAELKLDGVRNENLVQKQFPLSFTFGEALPPQYAKVLDELTDGKAI 480  
 DB 421 GNKKVLENRAELKLDGVRNENLVQKQFPLSFTFGEALPPQYAKVLDELTDGKAI 480  
 QY 481 ISTGVGQOMWAQFNYKPKQWLSGGLGANGFGFLPAAIGASVANPDAIWDIDGGS 540  
 DB 481 ISTGVGQOMWAQFNYKPKQWLSGGLGANGFGFLPAAIGASVANPDAIWDIDGGS 540  
 QY 541 FTMANVQELATIRVENLIPVKVLLNNQHLMGMQWEDRFYKANRAHTFLGDPAGEDEIPFN 600  
 DB 541 FTMANVQELATIRVENLIPVKVLLNNQHLMGMQWEDRFYKANRAHTFLGDPAGEDEIPFN 600  
 QY 601 MLFFAAACGIPAAVTKADLREAIQTWLDTPGPGYLLDVICPHQEHVLPMPNGGTFNDV 660

DB 601 MLFFAAACGIPAAVTKADLREAIQTWLDTPGPGYLLDVICPHQEHVLPMPNGGTFNDV 660  
 QY 661 ITEGGRIKY 670  
 DB 661 ITEGGRIKY 670  
 RESULT 2  
 AAE02400  
 ID AAE02400 standard; Protein; 670 AA.  
 XX AC  
 XX AAE02400;  
 XX AC  
 XX 10-AUG-2001 (first entry)  
 XX Arabidopsis thaliana acetolactate synthase mutant from plasmid pKS1.  
 DE Acetolactate synthase; ALS; imidazolinone-resistant; cytotoxic; mutant;  
 KW plasmid pKS1; crop plant; tobacco; herbicide; transgenic; mutin.  
 XX Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 XX Key Location/Qualifiers  
 FT Misc-difference 653 /note= "Wild type Ser substituted with Asn"  
 FT XX  
 XX US6225105-B1.  
 XX PN  
 XX 01-MAY-2001.  
 XX PD  
 XX 20-AUG-1998; 98US-0137478.  
 XX PF  
 XX 22-DEC-1994; 94US-0363208.  
 XX PR 15-FEB-1991; 91US-0657429.  
 XX PR 15-DEC-1992; 92US-0990416.  
 XX PR 27-JAN-1997; 97US-0789518.  
 XX PA (LOU) UNIV LOUISIANA STATE.  
 XX PI Sathasivan K, Murai N;  
 XX WPI; 2001-342398/36.  
 XX DR N-PSDB; AAD06570.  
 XX Novel bacterium comprising foreign imidazolinone-resistant acetolactate  
 PT synthase gene, useful for imparting imidazolinone resistance to crop  
 PT plant and as probe for isolation of mutated or wild-type ALS -  
 XX Claim 3; Fig 1; 19pp; English.  
 XX The present sequence is Arabidopsis thaliana imidazolinone-resistant  
 CC acetolactate synthase (ALS) enzyme mutant. Mutant ALS gene is isolated  
 CC from an imidazolinone-resistant Arabidopsis thaliana (GH-90) and stably  
 CC maintained in a plasmid pKS1. This mutant ALS is obtained by replacing  
 CC Ser with Asn at position 653. Mutant ALS gene is useful for imparting  
 CC imidazolinone resistance to a crop plant or for transforming crop plants  
 CC preferably tobacco, to protect host cells from the cytotoxic effects of  
 CC imidazolinone. Thus the imidazolinone resistance of the transformed crop  
 CC plant is greater than that of an untreated imidazolinone-sensitive wild-  
 CC type crop plant. Mutant ALS DNA is also used as a probe for isolating  
 CC mutated or wild-type ALS, and as a selective marker in plant  
 CC transformation systems with its native promoter in dicots and with a  
 CC modified promoter in monocots. Mutant ALS DNA permits the utilisation of  
 CC the imidazolinone or analogous herbicide as a single application at a  
 CC concentration which ensures the complete or substantially complete  
 CC killing of weeds, while leaving the transgenic crop plant essentially  
 CC undamaged.  
 XX SQ Sequence 670 AA;  
 Query Match 100.0%; Score 3448; DB 22; Length 670;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-278;

Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1	MAAATTTTSSISFSTKPSKSPSSKSPISRFSLPFLSLPNPKSSSSRRRGIKSSSPS 60
Db 1	MAAATTTTSSISFSTKPSKSPSSKSPISRFSLPFLSLPNPKSSSSRRRGIKSSSPS 60
QY 61	SISAVLNTTNTVTPSPKTKETETISRFAPDQPRKGADILVEALERQGVETVFAYPG 120
Db 61	SISAVLNTTNTVTPSPKTKETETISRFAPDQPRKGADILVEALERQGVETVFAYPG 120
QY 121	GASMEIHOALTRSSSINVLPRHQGVFAAGYARSSKPGICICATSPGATNLVSGLA 180
Db 121	GASMEIHOALTRSSSINVLPRHQGVFAAGYARSSKPGICICATSPGATNLVSGLA 180
QY 181	DALLDSVPLVAITQGVPRMIGTDAFQETPIVEVTRSTKHNVLVMDVEDIPRIIEA 240
Db 181	DALLDSVPLVAITQGVPRMIGTDAFQETPIVEVTRSTKHNVLVMDVEDIPRIIEA 240
QY 241	LATSGRPGVLDVDPKDIQQQLAIPNWEQAMRLPGVMSRMKPPEDSHLEQIVRLISESK 300
Db 241	LATSGRPGVLDVDPKDIQQQLAIPNWEQAMRLPGVMSRMKPPEDSHLEQIVRLISESK 300
QY 301	KPVLVYGGGCLNSDELGRFVELAGIPVASTLMGLGSPCCDELSLHMLGMGTYYANYA 360
Db 301	KPVLVYGGGCLNSDELGRFVELAGIPVASTLMGLGSPCCDELSLHMLGMGTYYANYA 360
QY 361	VEHSDLLAFGRFDRVTGKLEAFASRAKIVHIDISAEIGKNTKTHSVSGDVKLALQ 420
Db 361	VEHSDLLAFGRFDRVTGKLEAFASRAKIVHIDISAEIGKNTKTHSVSGDVKLALQ 420
QY 421	GKMKVLENRAELKIDFGVWENELNVOKFPLSKFTGEALPPQVAIKVLDLTDGKAI 480
Db 421	GKMKVLENRAELKIDFGVWENELNVOKFPLSKFTGEALPPQVAIKVLDLTDGKAI 480
QY 481	ISTVGQHQWAAQFYNNKPRQWSSGGLGAMGFLPAAGASVANPAIIVDIDGGS 540
Db 481	ISTVGQHQWAAQFYNNKPRQWSSGGLGAMGFLPAAGASVANPAIIVDIDGGS 540
QY 541	FIMVQELATIRVENLPVKVLLNNOHLGNWQWEDRYKANKRAHTFLGDPQAEDEIFPN 600
Db 541	FIMVQELATIRVENLPVKVLLNNOHLGNWQWEDRYKANKRAHTFLGDPQAEDEIFPN 600
QY 601	MLFAACGIPAAVTKKADIREAIQTMLDTPGPYLLDVI CPHQEHVLPMPNGGTNDV 660
Db 601	MLFAACGIPAAVTKKADIREAIQTMLDTPGPYLLDVI CPHQEHVLPMPNGGTNDV 660
QY 661	ITEGDGRIKY 670
Db 661	ITEGDGRIKY 670
RESULT 3	
AAW22457	
ID	AAW22457 standard; Protein; 670 AA.
AC	AAW22457;
DT	25-MAR-2003 (updated)
DT	25-SEP-1997 (first entry)
DE	Arabidopsis wild-type acetolactate synthase (sub-sequence C).
KW	Acetolactate synthase; ALS; herbicide resistance; transgenic plant;
KW	crop protection.
OS	Arabidopsis thaliana.
XX	
XX	Key Location/Qualifiers
FH	Peptide 1..90
FT	/label= Transit peptide
FT	/note= "putative" transit peptide extends for
FT	approx. 90 amino acids from N-terminal
FT	methionine residue"

XX	US5605011-A.
XX	25-FEB-1997.
XX	22-DEC-1994; 94US-0362022.
XX	27-JUL-1987; 87IL-0083348.
PR	04-MAR-1988; 88US-0164360.
PR	18-JAN-1991; 91US-0642976.
PR	26-AUG-1986; 86US-0900609.
PR	02-JUN-1992; 92US-0892305.
XX	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
PI	Yadav NS;
XX	WPI; 1997-153232/14.
DR	Use of mutant acetolactate synthase genes - for transforming plants
FT	for resistance to sulphonylurea, triazolopyrimidine sulphonamide
PT	and imidazolinone herbicides.
XX	Claim 1; Fig 6a-f; 63pp; English.
XX	Amino acid sub-sequences A-G respectively correspond to the large
CC	subunits of acetolactate synthase (ALS) isozymes I, II and III
CC	(AAW22459-61) from E. coli, and wild-type ALS proteins of yeast
CC	(AAW22458), Arabidopsis thaliana (AAW22457) and tobacco (AAW22455 and
CC	AAW22456). Comparison of these substantially conserved sequences
CC	with those of herbicide-resistant ALS enzymes (see also AAW22462-64)
CC	reveals the location of amino acid subunits. that lead to herbicide
CC	resistance. In sub-sequence C, such a subunit is located at the
CC	delta-2 position (any amino acid other than alanine). A nucleic
CC	acid encoding an ALS from any source can be mutated so that the
CC	encoded enzyme contains this amino acid subunit. Transformation of
CC	herbicide sensitive plants or plant cells with the nucleic acid
CC	results in resistance to the herbicide.
CC	(Updated on 25-MAR-2003 to correct PF field.)
CC	(Updated on 25-MAR-2003 to correct PR field.)
XX	Sequence 670 AA;
SQ	
Query Match 99.9%; Score 3443; DB 18; Length 670;	
Best Local Similarity 99.9%; Pred. No. 8e-278;	
Matches 669; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY 1	MAAATTTTSSISFSTKPSKSPSSKSPISRFSLPFLSLPNPKSSSSRRRGIKSSSPS 60
Db 1	MAAATTTTSSISFSTKPSKSPSSKSPISRFSLPFLSLPNPKSSSSRRRGIKSSSPS 60
QY 61	SISAVLNTTNTVTPSPKTKETETISRFAPDQPRKGADILVEALERQGVETVFAYPG 120
Db 61	SISAVLNTTNTVTPSPKTKETETISRFAPDQPRKGADILVEALERQGVETVFAYPG 120
QY 121	GASMEIHOALTRSSSINVLPRHQGVFAAGYARSSKPGICICATSPGATNLVSGLA 180
Db 121	GASMEIHOALTRSSSINVLPRHQGVFAAGYARSSKPGICICATSPGATNLVSGLA 180
QY 181	DALLDSVPLVAITQGVPRMIGTDAFQETPIVEVTRSTKHNVLVMDVEDIPRIIEA 240
Db 181	DALLDSVPLVAITQGVPRMIGTDAFQETPIVEVTRSTKHNVLVMDVEDIPRIIEA 240
QY 241	LATSGRPGVLDVDPKDIQQQLAIPNWEQAMRLPGVMSRMKPPEDSHLEQIVRLISESK 300
Db 241	LATSGRPGVLDVDPKDIQQQLAIPNWEQAMRLPGVMSRMKPPEDSHLEQIVRLISESK 300
QY 301	KPVLVYGGGCLNSDELGRFVELAGIPVASTLMGLGSPCCDELSLHMLGMGTYYANYA 360
Db 301	KPVLVYGGGCLNSDELGRFVELAGIPVASTLMGLGSPCCDELSLHMLGMGTYYANYA 360
QY 361	VEHSDLLAFGRFDRVTGKLEAFASRAKIVHIDISAEIGKNTKTHSVSGDVKLALQ 420

Db 361 VEHSDLLAGVDFDRVTKLEAFASRAKIVHIDIDSABEGKNTKTHSVSGDVKLALQ 420  
 Qy 421 GNNKYLENRAEELKLDGFWNRNELNVOKRFFLSFKTFGEAIPPOYAIVKVLDELTDGKAI 480  
 Db 421 GNNKYLENRAEELKLDGFWNRNELNVOKRFFLSFKTFGEAIPPOYAIVKVLDELTDGKAI 480  
 Qy 481 ISTGVGQHWAAQFYNYKKPQWMLSSGGLGANGFGLPAAGASVANPAIVVDIDGGS 540  
 Db 481 ISTGVGQHWAAQFYNYKKPQWMLSSGGLGANGFGLPAAGASVANPAIVVDIDGGS 540  
 Qy 541 FIMNVQELATIRVENLPVKVLLANNQHLGMVQWEDRFYKANRAHTFLGDPQAEDEIFPN 600  
 Db 541 FIMNVQELATIRVENLPVKVLLANNQHLGMVQWEDRFYKANRAHTFLGDPQAEDEIFPN 600  
 Qy 601 MLFPAACGIPPAARVTKKADIREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDV 660  
 Db 601 MLFPAACGIPPAARVTKKADIREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDV 660  
 Qy 661 ITEGDGRIKY 670  
 Db 661 ITEGDGRIKY 670

## RESULT 4

AAWS9146 standard; Protein; 670 AA.

XX ID AAW59146; AC AAW59146; DT 13-AUG-1998 (first entry)  
 XX DE A. thaliana acetolactate synthase protein.  
 XX KW Acetolactate synthase; ALS; imidazolinone resistance; herbicide; crop;  
 XX mutant; biosynthesis; valine; leucine; isoleucine; weed removal.  
 XX OS Arabidopsis thaliana.  
 XX PN US5767366-A.  
 XX PD 16-JUN-1998.  
 XX PF 22-DEC-1994; 94US-0363208.  
 XX PR 19-FEB-1991; 91US-0657429.  
 XX PR 15-DEC-1992; 92US-0990416.  
 XX PR 22-DEC-1994; 94US-0363208.  
 XX PA (LOU ) UNIV LOUISIANA STATE.  
 XX PI Murai N, Sathasivan K;  
 XX DR WPI; 1998-361818/31.  
 XX DR N-PSDB; AAV11890.

PT Imidazolinone resistant mutant acetolactate synthase gene - useful  
 for transforming plants and plant cells to confer resistance to the  
 herbicide

PS Disclosure; Page -; 20pp; English.

CC This sequence represents an Arabidopsis thaliana acetolactate  
 CC synthase (ALS) protein which is a key enzyme in the biosynthesis of  
 CC valine, leucine and isoleucine in plants. This enzyme is inhibited by  
 CC herbicides containing imidazolinone e.g. imazapyr, imazaquin and  
 CC imazepathyr. A mutant form of this enzyme, carrying a mutation where a  
 CC wild type Ser residue is replaced by an Asn at position 653 results  
 CC in an imidazolinone resistant ALS. Transformed plants and cells can be  
 CC used to confer imidazolinone resistance on crops, so the herbicide can be  
 CC be used in the removal of weeds. Current genetic engineering techniques  
 CC allow the transfer of the gene to different plant species. Traditional  
 CC imidazolinone resistance was only possible by classical breeding

CC techniques, which did not allow trait transfer out of a maize line.  
 CC Note: This wild type sequence does not appear in the specification but  
 CC has been made from the sequence represented in AAW59146.

SQ Sequence 670 AA;

Query Match 99.9%; Score 3443; DB 19; Length 670;

Best local similarity 99.9%; Pred. No. 8e-278;  
 Matches 66; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAATTTTSSISFSTKSPSSSKSPISRSFSLPNPNKSSSSRRRGKSSSPS 60  
 Db 1 MAATTTTSSISFSTKSPSSSKSPISRSFSLPNPNKSSSSRRRGKSSSPS 60  
 Qy 61 SISAVLNTTNTVTTSPSTKPTFISRFAPDQPKGADILVEALRQGVETVPAFG 120  
 Db 61 SISAVLNTTNTVTTSPSTKPTFISRFAPDQPKGADILVEALRQGVETVPAFG 120  
 Qy 121 GASMEHQALTRSSSIRNVLPRHGGVFAAEGVARSCKPGICATSGPATNLVSGLA 180  
 Db 121 GASMEHQALTRSSSIRNVLPRHGGVFAAEGVARSCKPGICATSGPATNLVSGLA 180  
 Qy 181 DALLDSVPLVAITQVPRRMIGTDAFOETPIVEVTRITKHNYLVMDVEDIPRIIEAFF 240  
 Db 181 DALLDSVPLVAITQVPRRMIGTDAFOETPIVEVTRITKHNYLVMDVEDIPRIIEAFF 240  
 Qy 241 LATSGRPGVLVDVPKDIQQOLAI PNWQAMRLPGYMSRMPKPPEDSHLEQIVELISESK 300  
 Db 241 LATSGRPGVLVDVPKDIQQOLAI PNWQAMRLPGYMSRMPKPPEDSHLEQIVELISESK 300  
 Qy 301 KPYLYVGGCINSSDELGRFVELTGIPVASTLMGLSGYPCDDDELSLHMLGNHGTVYANYA 360  
 Db 301 KPYLYVGGCINSSDELGRFVELTGIPVASTLMGLSGYPCDDDELSLHMLGNHGTVYANYA 360  
 Qy 361 VEHSDLLAGVDFDRVTKLEAFASRAKIVHIDIDSABEGKNTKTHSVSGDVKLALQ 420  
 Db 361 VEHSDLLAGVDFDRVTKLEAFASRAKIVHIDIDSABEGKNTKTHSVSGDVKLALQ 420  
 Qy 421 GNNKYLENRAEELKLDGFWNRNELNVOKRFFLSFKTFGEAIPPOYAIVKVLDELTDGKAI 480  
 Db 421 GNNKYLENRAEELKLDGFWNRNELNVOKRFFLSFKTFGEAIPPOYAIVKVLDELTDGKAI 480  
 Qy 481 ISTGVGQHWAAQFYNYKKPQWMLSSGGLGANGFGLPAAGASVANPAIVVDIDGGS 540  
 Db 481 ISTGVGQHWAAQFYNYKKPQWMLSSGGLGANGFGLPAAGASVANPAIVVDIDGGS 540  
 Qy 541 FIMNVQELATIRVENLPVKVLLANNQHLGMVQWEDRFYKANRAHTFLGDPQAEDEIFPN 600  
 Db 541 FIMNVQELATIRVENLPVKVLLANNQHLGMVQWEDRFYKANRAHTFLGDPQAEDEIFPN 600  
 Qy 601 MLFPAACGIPPAARVTKKADIREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDV 660  
 Db 601 MLFPAACGIPPAARVTKKADIREAIQTMLDTPGPYLLDVICPHQEHVLPMPNGGTFNDV 660  
 Qy 661 ITEGDGRIKY 670  
 Db 661 ITEGDGRIKY 670

## RESULT 5

AAWS4287 standard; Protein; 670 AA.

XX ID AAG54287; AC AAG54287; DT 18-OCT-2000 (first entry)  
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 69201.  
 XX KW Protein identification; signal transduction pathway; metabolic pathway;  
 XX hybridisation assay; genetic mapping; gene expression control; promoter;  
 XX termination sequence.

OS Arabidopsis thaliana.  
XX EF1033405-A2.  
XX 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
XX 05-MAR-1999; 99US-0123180.  
XX 03-MAR-1999; 99US-0123548.  
XX 23-MAR-1999; 99US-0125788.  
XX 25-MAR-1999; 99US-0126264.  
XX 29-MAR-1999; 99US-0126785.  
XX 01-APR-1999; 99US-0127462.  
XX 06-APR-1999; 99US-0128234.  
XX 08-APR-1999; 99US-0128714.  
XX 16-APR-1999; 99US-0129845.  
XX 19-APR-1999; 99US-0130077.  
XX 21-APR-1999; 99US-0130449.  
XX 23-APR-1999; 99US-0130510.  
XX 23-APR-1999; 99US-0130891.  
XX 28-APR-1999; 99US-0131449.  
XX 30-APR-1999; 99US-0132048.  
XX 04-MAY-1999; 99US-0132407.  
XX 05-MAY-1999; 99US-0132484.  
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XX 06-MAY-1999; 99US-0132486.  
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XX 14-MAY-1999; 99US-0134218.  
XX 14-MAY-1999; 99US-0134219.  
XX 14-MAY-1999; 99US-0134221.  
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XX 27-MAY-1999; 99US-0136392.  
XX 28-MAY-1999; 99US-0136782.  
XX 01-JUN-1999; 99US-0137222.  
XX 03-JUN-1999; 99US-0137528.  
XX 04-JUN-1999; 99US-0137502.  
XX 07-JUN-1999; 99US-0137724.  
XX 08-JUN-1999; 99US-0138094.  
XX 10-JUN-1999; 99US-0138540.  
XX 10-JUN-1999; 99US-0138847.  
XX 14-JUN-1999; 99US-0139119.  
XX 16-JUN-1999; 99US-0139452.  
XX 16-JUN-1999; 99US-0139453.  
XX 17-JUN-1999; 99US-0139492.  
XX 18-JUN-1999; 99US-0139454.  
XX 18-JUN-1999; 99US-0139455.  
XX 18-JUN-1999; 99US-0139456.  
XX 18-JUN-1999; 99US-0139457.  
XX 18-JUN-1999; 99US-0139458.  
XX 18-JUN-1999; 99US-0139459.  
XX 18-JUN-1999; 99US-0139460.  
XX 18-JUN-1999; 99US-0139461.  
XX 18-JUN-1999; 99US-0139462.  
XX 18-JUN-1999; 99US-0139463.  
XX 18-JUN-1999; 99US-0139750.  
XX 18-JUN-1999; 99US-0139763.  
XX 21-JUN-1999; 99US-0139817.  
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XX 23-JUN-1999; 99US-0140353.  
XX 23-JUN-1999; 99US-0140354.  
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XX 28-JUN-1999; 99US-0140823.  
XX 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
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PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
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PR 20-JUL-1999; 99US-0144884.  
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PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
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PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151055.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.

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PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 23-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
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PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 99.9%; Score 3443; DB 21; Length 670;
Best Local Similarity 99.9%; Pred. No. 8e-278;
Matches 669; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAATTTTSSISSTKSPSSSKSLPTISRSFSPFLSPNKSSSSRRGKSSSPS 60
DB 1 MAAATTTTSSISSTKSPSSSKSLPTISRSFSPFLSPNKSSSSRRGKSSSPS 60

QY 61 SISAVLNTTNTVTTSPKTPKPTFTISRPADQPRKGADILVEALERQGVETVAYFG 120
DB 61 SISAVLNTTNTVTTSPKTPKPTFTISRPADQPRKGADILVEALERQGVETVAYFG 120

QY 121 GASMEIHOALTRSSRNVLPRHEGGVFAAGYARSSCKPGICATSGCATNLVSLGA 180
DB 121 GASMEIHOALTRSSRNVLPRHEGGVFAAGYARSSCKPGICATSGCATNLVSLGA 180

QY 181 DALLDSVPLVAITGOVPRRMIGTDAQETPIVEVTRSIKHNLMVMDVEDIPRIIEAFF 240
DB 181 DALLDSVPLVAITGOVPRRMIGTDAQETPIVEVTRSIKHNLMVMDVEDIPRIIEAFF 240

QY 241 LATSGRPGVLDVYDKDIOQOALNPNQALNPGYMSRMPKPPEDSHLOIVRLISSEK 300
DB 241 LATSGRPGVLDVYDKDIOQOALNPNQALNPGYMSRMPKPPEDSHLOIVRLISSEK 300

QY 301 KPVLYVGGCLNSDELGRVELTGIPVASTLMGLGSYPCDDLSLMLGMHGVYANYA 360
DB 301 KPVLYVGGCLNSDELGRVELTGIPVASTLMGLGSYPCDDLSLMLGMHGVYANYA 360

QY 361 VHSDDLILAFGRFDRVTGKLEAFASPAKIVHIDIDSAEIGKNTPHSVSCGDVKLAIQ 420

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DB 361 VHSDDLILAFGRFDRVTGKLEAFASPAKIVHIDIDSAEIGKNTPHSVSCGDVKLAIQ 420
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DB 421 GMMKYLENRAEELKLDPGVWRNELNVQKFPJLSFKTFGEAIPPOYAIAKVLDELTDGKAI 480
QY 481 ISTGVGOHMAAOFYNNYKPKRWLSGGGLGAMGFGLPAAIGASVANPDALVVDIDGGS 540
DB 481 ISTGVGOHMAAOFYNNYKPKRWLSGGGLGAMGFGLPAAIGASVANPDALVVDIDGGS 540
QY 541 FIMNVOELATIRVENLPVKVLLLNNOHLGMVMOEDRFYKANRAHTFLGDPADREIFPN 600
DB 541 FIMNVOELATIRVENLPVKVLLLNNOHLGMVMOEDRFYKANRAHTFLGDPADREIFPN 600
QY 601 MLFPAACGIPAAVTKADLREAIQTMIDTPGGLDVTCPHQSHVLPMPINGSTFNDV 660
DB 601 MLFPAACGIPAAVTKADLREAIQTMIDTPGGLDVTCPHQSHVLPMPINGSTFNDV 660
QY 661 ITEGDGRIKY 670
DB 661 ITEGDGRIKY 670

RESULT 6
AAOI5640
ID AAOI5640 standard; Protein; 670 AA.
XX
AC AAOI5640;
XX
DT 08-NOV-2002 (first entry)
XX
DE Modified Arabidopsis thaliana acetoxyhydroxyacid synthase (AHAS) protein.
XX
RW AHAS; mutein; mutant; acetoxyhydroxyacid synthase; weed control;
XX transgenic tree; imidazolinone herbicide resistance; transgenic seed.
XX
OS Arabidopsis thaliana.
XX
PH Key Location/Qualifiers
FT Misc-difference 503 /note= "Encoded by CAG; The residue is represented as O
FT in the specification"
XX
PN WC200258459-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WC-US02331.
XX
PR 25-JAN-2001; 2001US-264216P.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Karnosky DF, Podila G, Xiang B;
XX
PI PI; 2002-608393/65.
XX
PI N-PSDB; AAL44391.
XX
New transgenic tree cell with altered acetoxyhydroxyacid synthase, useful
for producing imidazolinone-resistant transgenic seeds or trees, which
are important when imidazolinone herbicide is used to control weeds in
the vicinity
XX
PS Claim 6; Fig 1C; 32pp; English.
XX
CC The invention comprises a transgenic tree cell, which is transformed by
an altered acetoxyhydroxyacid synthase (AHAS) gene. Expression of the AHAS
nucleic acid in the tree cell results in increased resistance to an
imidazolinone herbicide as compared to a wild type variety of the tree
cell. The transgenic tree cell is useful for producing transgenic seeds
or trees having increased resistance to an imidazolinone herbicide. The
transgenic cell, seed or trees are useful in agriculture, particularly

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CC when imidazolinone herbicide is employed using spray over techniques to  
CC control weeds within the vicinity. The present amino acid sequence  
CC represents a modified version of the Arabidopsis thaliana AHAS protein.  
XX  
SQ Sequence 670 AA;  
Query Match 99.8%; Score 3442; DB 23; Length 670;  
Best Local Similarity 99.9%; Pred. No. 9.7e-278;  
Matches 669; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAATTTTSSISFSTKPSKSPSSKSPDIPRSLPFLPNPKSSSSRRRGKISSPS 60  
DB 1 MAATTTTSSISFSTKPSKSPSSKSPDIPRSLPFLPNPKSSSSRRRGKISSPS 60  
QY 61 SISAVLNTTNTVTPSTKPTKPTETIFGRFAPDQPRKADILVEALERQGVETVFAYPG 120  
DB 61 SISAVLNTTNTVTPSTKPTKPTETIFGRFAPDQPRKADILVEALERQGVETVFAYPG 120  
QY 121 GASMEIHOALTRSSISIRNVLPREOGGVFAAGYARSSGKPGICATSGCATNLVSGLA 180  
DB 121 GASMEIHOALTRSSISIRNVLPREOGGVFAAGYARSSGKPGICATSGCATNLVSGLA 180  
QY 181 DALLDSVPLVAITGVPRMIGTDAFOETPIVEVTRSTKHNVLVMDVEDIPRIIEAFA 240  
DB 181 DALLDSVPLVAITGVPRMIGTDAFOETPIVEVTRSTKHNVLVMDVEDIPRIIEAFA 240  
QY 241 LATSGRGPVLVDVVKDIOQOLAI PNWQAMRLPGYMSRMPKPPDSHLEQIVRLISESK 300  
DB 241 LATSGRGPVLVDVVKDIOQOLAI PNWQAMRLPGYMSRMPKPPDSHLEQIVRLISESK 300  
QY 301 KPVLYVGGCLNSSLDELGRFVELTGIPVASTLMGLGSPCDDELSTLHMLGMHGTVYANYA 360  
DB 301 KPVLYVGGCLNSSLDELGRFVELTGIPVASTLMGLGSPCDDELSTLHMLGMHGTVYANYA 360  
QY 361 VEHSDLLAFGRVFRDRTVTKLEAFASRAKIVHIDISAEIGKNTKTPHVSVCVDVLAQ 420  
DB 361 VEHSDLLAFGRVFRDRTVTKLEAFASRAKIVHIDISAEIGKNTKTPHVSVCVDVLAQ 420  
QY 421 GNNKVLNRAEELKLDGFWNRNVLNVRQKFFLSFKTFGEAIPPOYAIKVLDLTDGKAI 480  
DB 421 GNNKVLNRAEELKLDGFWNRNVLNVRQKFFLSFKTFGEAIPPOYAIKVLDLTDGKAI 480  
QY 481 ISTGVGQHWAQAFYNYKPRQWSSGGLGAMGFLPAAGASVANDPAIVVDIDGDS 540  
DB 481 ISTGVGQHWAQAFYNYKPRQWSSGGLGAMGFLPAAGASVANDPAIVVDIDGDS 540  
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DB 541 FTMNVQELATIRVENLPVKVLLANNQHLGNVQWEDRFYKANRAHTFLGDPQAEDEIFPN 600  
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DB 601 MLLFAAACGIPAAVTKKADIREAIQTNLDTGPIVLLVIPCPOHEHVLPMIPNGGTNDV 660  
QY 661 ITEGDEGRIKY 670  
DB 661 ITEGDEGRIKY 670  
RESULT 7  
AAR11975  
ID AAR11975 standard; Protein; 670 AA.  
XX AC AAR11975;  
XX DT 25-MAR-2003 (updated)  
XX DT 25-JUL-1991 (first entry)  
XX DE Tobacco herbicide-resistant acetolactate synthase.  
XX KW Tobacco; acetolactate synthase, ALS; herbicide; resistance.  
XX OS Arabidopsis.

XX  
FH Key Location/Qualifiers  
FT CDS 506..2515  
FT /\*tag= a  
FT /product= ALS  
XX US5013659-A.  
XX 07-MAY-1991.  
XX 04-MAR-1988; 88US-0164360.  
XX 04-MAR-1988; 88US-0164360.  
XX 26-AUG-1986; 86US-0900609.  
XX (DUPO) DU PONT DE NEMOURS & CO E I.  
XX Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR,  
XX Yadav NS;  
XX WPI; 1991-156075/21.  
XX N-FSDS; AAQ11496.  
XX Nucleic acid fragment - encoding herbicide-resistant plant  
XX aceto:lactate synthase protein  
XX Disclosure; Fig 10; 65; English.  
XX The protein can confer resistance to chlorsulfuron up to 30 ppb  
XX in transformed tobacco calluses.  
XX See also AAQ11495-6.  
XX (Updated on 25-MAR-2003 to correct PA field.)  
XX Sequence 670 AA;  
Query Match 99.6%; Score 3435; DB 12; Length 670;  
Best Local Similarity 99.7%; Pred. No. 3.7e-277;  
Matches 668; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAATTTTSSISFSTKPSKSPSSKSPDIPRSLPFLPNPKSSSSRRRGKISSPS 60  
DB 1 MAATTTTSSISFSTKPSKSPSSKSPDIPRSLPFLPNPKSSSSRRRGKISSPS 60  
QY 61 SISAVLNTTNTVTPSTKPTKPTETIFSRFAPDQPRKADILVEALERQGVETVFAYPG 120  
DB 61 SISAVLNTTNTVTPSTKPTKPTETIFSRFAPDQPRKADILVEALERQGVETVFAYPG 120  
QY 121 GASMEIHOALTRSSISIRNVLPREOGGVFAAGYARSSGKPGICATSGCATNLVSGLA 180  
DB 121 GASMEIHOALTRSSISIRNVLPREOGGVFAAGYARSSGKPGICATSGCATNLVSGLA 180  
QY 181 DALLDSVPLVAITGVPRMIGTDAFOETPIVEVTRSTKHNVLVMDVEDIPRIIEAFA 240  
DB 181 DALLDSVPLVAITGVPRMIGTDAFOETPIVEVTRSTKHNVLVMDVEDIPRIIEAFA 240  
QY 241 LATSGRGPVLVDVVKDIOQOLAI PNWQAMRLPGYMSRMPKPPDSHLEQIVRLISESK 300  
DB 241 LATSGRGPVLVDVVKDIOQOLAI PNWQAMRLPGYMSRMPKPPDSHLEQIVRLISESK 300  
QY 301 KPVLYVGGCLNSSLDELGRFVELTGIPVASTLMGLGSPCDDELSTLHMLGMHGTVYANYA 360  
DB 301 KPVLYVGGCLNSSLDELGRFVELTGIPVASTLMGLGSPCDDELSTLHMLGMHGTVYANYA 360  
QY 361 VEHSDLLAFGRVFRDRTVTKLEAFASRAKIVHIDISAEIGKNTKTPHVSVCVDVLAQ 420  
DB 361 VEHSDLLAFGRVFRDRTVTKLEAFASRAKIVHIDISAEIGKNTKTPHVSVCVDVLAQ 420  
QY 421 GNNKVLNRAEELKLDGFWNRNVLNVRQKFFLSFKTFGEAIPPOYAIKVLDLTDGKAI 480  
DB 421 GNNKVLNRAEELKLDGFWNRNVLNVRQKFFLSFKTFGEAIPPOYAIKVLDLTDGKAI 480  
QY 481 ISTGVGQHWAQAFYNYKPRQWSSGGLGAMGFLPAAGASVANDPAIVVDIDGDS 540  
DB 481 ISTGVGQHWAQAFYNYKPRQWSSGGLGAMGFLPAAGASVANDPAIVVDIDGDS 540

Db 481 ISTGVGQWAAQFNYKKPROMLSSGGLGANGRLPAALGASVANPDAIVVDIDGGS 540  
 QY 541 FIMVQELATIRVENLPVKVLLNNHLMGMWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600  
 Db 541 FIMVQELATIRVENLPVKVLLNNHLMGMWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600  
 QY 601 MLLFAACGIPPAARVTKKADLREAIQTMLDTFGPYLLDVICPHQHVLPMPINGGTFNDV 660  
 Db 601 MLLFAACGIPPAARVTKKADLREAIQTMLDTFGPYLLDVICPHQHVLPMPINGGTFNDV 660  
 QY 661 ITEGDGRIKY 670  
 Db 661 ITEGDGRIKY 670

RESULT 8  
 AAR63082  
 ID AAR63082 standard; Protein; 670 AA.  
 AC AAR63082;  
 XX AAR63082;  
 DT 25-MAR-2003 (updated)  
 DT 12-FEB-1993 (first entry)  
 XX 25-MAR-2003 (updated)  
 XX 12-FEB-1993 (first entry)  
 DE ALS mutant of Arabidopsis.  
 XX Herbicide resistant; acetolactate synthase; ALS; sulphonylurea;  
 KW triazolopyrimidinesulphonamide; imidazolinone; markers.  
 XX Arabidopsis thaliana.  
 XX US5141870-A.  
 XX 25-AUG-1992.  
 XX 18-JAN-1991; 91US-0642976.  
 XX 26-AUG-1986; 86US-0900609.  
 PR 04-MAR-1988; 88US-0164360.  
 PR 18-JAN-1991; 91US-0642976.  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;  
 PI Yadav NS;  
 XX KPI; 1992-307863/37.  
 DR N-PSDB; AAQ26913.  
 XX Conferring herbicide resistance on plants - using a nucleic acid  
 PT fragment encoding a herbicide-resistant plant aceto:lactate  
 PT synthase protein  
 XX Disclosure; Fig 10; 63pp; English.  
 CC The sequence was deduced from a mutant acetolactate synthetase gene  
 CC isolated from herbicide resistant strains of Arabidopsis thaliana.  
 CC designated GH50. The GH50 mutant ALS gene may be isolated from  
 CC Arabidopsis plants resistant to sulphonylurea, triazolopyrimidine  
 CC sulphonamide and imidazolinone herbicides. The gene may be used to  
 CC transform plants to confer herbicide resistance to plants such as  
 CC tobacco, petunia, cotton, sugarbeet, potato, tomato, lettuce,  
 CC sunflower, soybean, corn, wheat, rice, poplars, alfalfa, oats, etc.  
 CC The herbicide resistant ALS genes can also be used as markers for  
 CC transformation of an organism by a second DNA fragment.  
 CC See also AAR26911-2.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 670 AA;

Query Match 99.68; Score 3435; DB 13; Length 670;

Best Local Similarity 99.74; Pred. No. 3.7e-277;

Matches 668; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAATTTTTTSSSISFTKSPSSSSKSPISRSPLPFSINPNKSSSSRRRGIKSSSPS 60  
 Db 1 MAATTTTTTSSSISFTKSPSSSSKSPISRSPLPFSINPNKSSSSRRRGIKSSSPS 60  
 QY 61 SISAVLNTTNTTTPSTKPTKPTFTISRFAPDQPKGADILVEALERQGVETVAYPG 120  
 Db 61 SISAVLNTTNTTTPSTKPTKPTFTISRFAPDQPKGADILVEALERQGVETVAYPG 120  
 QY 121 GASMEIHOALTRSSSINVLPRHEOGGVFAAEGYARSSGKPGICIATSPGATNLVSGLA 180  
 Db 121 GASMEIHOALTRSSSINVLPRHEOGGVFAAEGYARSSGKPGICIATSPGATNLVSGLA 180  
 QY 181 DALDSVPLVAITGVPRRMIGTDAFOETPIVETSIKHNVLVMDVEDIPRIIEAFF 240  
 Db 181 DALDSVPLVAITGVPRRMIGTDAFOETPIVETSIKHNVLVMDVEDIPRIIEAFF 240  
 QY 241 LATSGRPGVPLVDVFKDIOQOLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVELISESK 300  
 Db 241 LATSGRPGVPLVDVFKDIOQOLAIPNWEQAMRLPGYMSRMPKPPEDSHLEQIVELISESK 300  
 QY 301 KPYLYVGGGCLNSSLDELGRFVELTGI PVASTLMGLGSGYPCDDDELHMLGMHGTVANYA 360  
 Db 301 KPYLYVGGGCLNSSLDELGRFVELTGI PVASTLMGLGSGYPCDDDELHMLGMHGTVANYA 360  
 QY 361 VEHSDLLAFVGRFDDRVTKLEAFASRAKIVHIDIDSABIGKNTKTPHVSVCGBVKLALQ 420  
 Db 361 VEHSDLLAFVGRFDDRVTKLEAFASRAKIVHIDIDSABIGKNTKTPHVSVCGBVKLALQ 420  
 QY 421 GNMKVLNRAEELKLDGFWWENELNVOKFPLSKFTFGAIPPOVAIKVLDLTDGKAI 480  
 Db 421 GNMKVLNRAEELKLDGFWWENELNVOKFPLSKFTFGAIPPOVAIKVLDLTDGKAI 480  
 QY 481 ISTGVGQWAAQFNYKKPROMLSSGGLGANGRLPAALGASVANPDAIVVDIDGGS 540  
 Db 481 ISTGVGQWAAQFNYKKPROMLSSGGLGANGRLPAALGASVANPDAIVVDIDGGS 540  
 QY 541 FIMVQELATIRVENLPVKVLLNNHLMGMWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600  
 Db 541 FIMVQELATIRVENLPVKVLLNNHLMGMWQWEDRFYKANRAHTFLGDPQAEDEIFPN 600  
 QY 601 MLLFAACGIPPAARVTKKADLREAIQTMLDTFGPYLLDVICPHQHVLPMPINGGTFNDV 660  
 Db 601 MLLFAACGIPPAARVTKKADLREAIQTMLDTFGPYLLDVICPHQHVLPMPINGGTFNDV 660  
 QY 661 ITEGDGRIKY 670  
 Db 661 ITEGDGRIKY 670

RESULT 9  
 AAR63082  
 ID AAR63082 standard; Protein; 670 AA.  
 AC AAR63082;  
 XX AAR63082;  
 DT 25-MAR-2003 (updated)  
 DT 16-AUG-1995 (first entry)  
 XX Herbicide-resistant ALS (P197A).  
 XX Acetolactate-synthase; ALS; herbicide-resistance; tobacco;  
 KW transgenic plant; crop improvement; chlorsulfuron;  
 KW sulfometuron methyl; mutagenesis; SUPA-C3 gene.  
 XX Arabidopsis thaliana.  
 OS US5378824-A.  
 XX 03-JUN-1995.  
 XX 02-JUN-1992; 92US-0892305.



PR 27-JUL-1987; 87IL-0083348.  
 PR 04-MAR-1988; 88US-0164360.  
 PR 18-JAN-1991; 91US-0642976.  
 PR 26-AUG-1986; 86US-0900609.  
 XX  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX  
 XX Chaleff RS, Yadav NS, Mazur BJ, Falco SC, Somerville CR;  
 PI Bedbrook JR;  
 XX  
 DR WPI; 1995-065894/09.  
 DR N-PSDB; AAQ81183.  
 XX  
 PT Nucleic acid fragment encoding a plant acetolactate synthase -  
 PT confers herbicide resistance when introduced to  
 PT herbicide-sensitive plants  
 XX  
 XX Disclosure; Fig. 10A-10D; 62pp; English.  
 XX  
 CC Sulfonylurea-resistant mutants of Arabidopsis thaliana were  
 CC obtained following ethyl methane sulfonate mutagenesis of seeds.  
 CC The mutant acetolactate-synthase (ALS) gene (given in AAQ81183) was  
 CC identified from a genomic DNA library in phage lambda. The  
 CC encoded ALS (AA863082) carried a P197A mutation, leading to improved  
 CC resistance to chlor-sulfuron and sulfometuron methyl herbicides.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 670 AA;  
 Query Match 99.6%; Score 3435; DB 16; Length 670;  
 Best Local Similarity 99.7%; Pred. No. 3.7e-277;  
 Matches 668; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAATTTTTSSSISFSTKPSSSKSPLEISFSLPFLNPNKSSRRRGKSSSPS 60  
 DB 1 MAATTTTTSSSISFSTKPSSSKSPLEISFSLPFLNPNKSSRRRGKSSSPS 60  
 QY 61 SISAVNTNTNTTSPKPTKPTETISFPADPRKADILVEALERQGVETVFPYG 120  
 DB 61 SISAVNTNTNTTSPKPTKPTETISFPADPRKADILVEALERQGVETVFPYG 120  
 QY 121 GASMEIHQALTRSSIRNVLPRHEGGVFAAGYARSSGKFGICATSPGATNLVSLA 180  
 DB 121 GASMEIHQALTRSSIRNVLPRHEGGVFAAGYARSSGKFGICATSPGATNLVSLA 180  
 QY 181 DALLDSVPLVALTGOVPRWIGTDAFOETPIVEVTSITKKNYLWMDVEDPIRIEFAFF 240  
 DB 181 DALLDSVPLVALTGOVPRWIGTDAFOETPIVEVTSITKKNYLWMDVEDPIRIEFAFF 240  
 QY 241 LATSGRPGVLVDPKDIQQQALIPNWEQAMLPFGYMSMPKPPEDSHLEQIVRLISESK 300  
 DB 241 LATSGRPGVLVDPKDIQQQALIPNWEQAMLPFGYMSMPKPPEDSHLEQIVRLISESK 300  
 QY 301 KEVLVVGCCCLNSDSHGLGFVELTGPVASTMGLGSYCDDELHMLGHWGTWYANYA 360  
 DB 301 KEVLVVGCCCLNSDSHGLGFVELTGPVASTMGLGSYCDDELHMLGHWGTWYANYA 360  
 QY 361 VEHSDLLAAGVFPDRDRTVKLEAPASRAKIVHIDIDSATIGKNTPHSVGCVKALQ 420  
 DB 361 VEHSDLLAAGVFPDRDRTVKLEAPASRAKIVHIDIDSATIGKNTPHSVGCVKALQ 420  
 QY 421 GNNKVLNRAELKLDGFWRNELNVOKFPLSFKTRGEAIPOYAIKVLDELIDGKAI 480  
 DB 421 GNNKVLNRAELKLDGFWRNELNVOKFPLSFKTRGEAIPOYAIKVLDELIDGKAI 480  
 QY 481 ISTGVGHQWMAAQFYNNKKPQWLSSGGLGAMGFLPAATIGASVANPDAIVVDIDGGS 540  
 DB 481 ISTGVGHQWMAAQFYNNKKPQWLSSGGLGAMGFLPAATIGASVANPDAIVVDIDGGS 540  
 QY 541 FTMVQELATIRVENLPVKVILLNNOHLGMVQWEDRFYKANRAHTFLGDPAQEDIEFPN 600

DB 541 FTMVQELATIRVENLPVKVILLNNOHLGMVQWEDRFYKANRAHTFLGDPAQEDIEFPN 600  
 QY 601 MLLEFAACGIPAARVYTKADLREAIQTMLTPGPYLLDVI CPHQSHVLPMPINGGTFNVDV 660  
 DB 601 MLLEFAACGIPAARVYTKADLREAIQTMLTPGPYLLDVI CPHQSHVLPMPINGGTFNVDV 660  
 QY 661 ITEGDRIKY 670  
 DB 661 ITEGDRIKY 670  
 RESULT 10  
 AAW22464  
 ID AAW22464 standard; Protein; 670 AA.  
 XX  
 AC AAW22464;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 25-SEP-1997 (first entry)  
 XX  
 DE Arabidopsis herbicide resistant acetolactate synthase.  
 XX  
 KW Acetolactate synthase; ALS; herbicide resistance; transgenic plant;  
 crop protection.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 FN US5605011-A.  
 XX  
 PD 25-FEB-1997.  
 XX  
 PF 22-DEC-1994; 94US-0362022.  
 PR 27-JUL-1987; 87IL-0083348.  
 PR 04-MAR-1988; 88US-0164360.  
 PR 18-JAN-1991; 91US-0642976.  
 PR 26-AUG-1986; 86US-0900609.  
 PR 02-JUN-1992; 92US-0892305.  
 XX  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;  
 Yadav NS;  
 XX  
 DR WPI; 1997-153232/14.  
 DR N-PSDB; AAT72864.  
 XX  
 PT Use of mutant acetolactate synthase genes - for transforming plants  
 PT for resistance to sulfonylurea, triazopyrimidine sulphonamide  
 PT and imidazolinone herbicides.  
 XX  
 PS Disclosure; Fig 10; 63pp; English.  
 XX  
 CC An Arabidopsis thaliana mutant acetolactate synthases (ALS)  
 CC (AAW22463) shows higher resistance to the sulfonylurea herbicides  
 CC chlor-sulfuron and sulfometuron methyl than the wild-type ALS (see  
 CC also AAW22457). The mutant enzyme carries a single Pro to Ser  
 CC substn. at the alpha-1 position in comparison to the wild-type  
 CC enzyme. A nucleic acid encoding an ALS from any biological source  
 CC can be mutated so that the encoded enzyme contains an amino acid  
 CC substn. at this position. Transformation of herbicide sensitive  
 CC plants or plant cells with the nucleic acid results in resistance  
 CC to the herbicide.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 670 AA;  
 Query Match 99.6%; Score 3435; DB 18; Length 670;  
 Best Local Similarity 99.7%; Pred. No. 3.7e-277;  
 Matches 668; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAATTTTTSSSISFSTKPSSSKSPLEISFSLPFLNPNKSSRRRGKSSSPS 60

Db 1 MAAATTTTSSSSISFKPSSSKSPLFISFSLPNSKSSSSRRRGKSSSPS 60  
 QY 61 SISAVLNTNTNTTSPSTKPTETISRFAPDQPRKGADILVEALERQGVETVFAYPG 120  
 Db 61 SISAVLNTNTNTTSPSTKPTETISRFAPDQPRKGADILVEALERQGVETVFAYPG 120  
 QY 121 GASMEIHOALTTRSSISRNVLPRHQGVFAAGYARSSKPGICGICATSPGATNLVSGLA 180  
 Db 121 GASMEIHOALTTRSSISRNVLPRHQGVFAAGYARSSKPGICGICATSPGATNLVSGLA 180  
 QY 181 DALLDSVPLVAITGVQPRRMIGTDAFOETPIVEVTRSTIKENYLVMDVEDIPRIIEBAFF 240  
 Db 181 DALLDSVPLVAITGVQPRRMIGTDAFOETPIVEVTRSTIKENYLVMDVEDIPRIIEBAFF 240  
 QY 241 LATSGRPGVLVDVFKDIOQOLAI PNWQAMRLPGYMSRMKPPEDSHLEQIVRLISESK 300  
 Db 241 LATSGRPGVLVDVFKDIOQOLAI PNWQAMRLPGYMSRMKPPEDSHLEQIVRLISESK 300  
 QY 301 KPVLYVGGGCLNSDELGRFVELTGIPVASTLMLGSGYPCDDDELSTHMLGMEGTVYANYA 360  
 Db 301 KPVLYVGGGCLNSDELGRFVELTGIPVASTLMLGSGYPCDDDELSTHMLGMEGTVYANYA 360  
 QY 361 VEHSDLLAFGVFRDRTVTKLEAFASRAKIVHIDISAEIGKNTPHVSGDVYKALQ 420  
 Db 361 VEHSDLLAFGVFRDRTVTKLEAFASRAKIVHIDISAEIGKNTPHVSGDVYKALQ 420  
 QY 421 GNMKVLNRAEELKLDGFWNRNELNVQKFPPLSPKTFGEAIPPOYAIKVLDELTDGKAI 480  
 Db 421 GNMKVLNRAEELKLDGFWNRNELNVQKFPPLSPKTFGEAIPPOYAIKVLDELTDGKAI 480  
 QY 481 ISTGVGHQWMAAOFYNYKKPRLNNOHLMGMWOWEDRFYKANRAHTFLGDPACDEIFPN 600  
 Db 481 ISTGVGHQWMAAOFYNYKKPRLNNOHLMGMWOWEDRFYKANRAHTFLGDPACDEIFPN 600  
 QY 601 MLLFAAACGIPAAVTVTKADIREALQTMLDTPGTYLLDVI CPHQEHVLPMPISGTFENDV 660  
 Db 601 MLLFAAACGIPAAVTVTKADIREALQTMLDTPGTYLLDVI CPHQEHVLPMPISGTFENDV 660

## RESULT 11

AAR24800 standard; Protein; 669 AA.

XX AAR24800;

XX 25-MAR-2003 (updated)

DT 11-DEC-1992 (first entry)

XX Ser653 deleted acetohydroxy acid synthase.

DE AHAS; herbicide resistance; plants; imidazolinones;

XX triazolopyrimidines; sulphonylureas.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX EP492113-A2.

XX 01-JUL-1992.

XX 12-NOV-1991; 91EP-0119254.

XX 27-DEC-1990; 90US-0633210.

XX (AMCY ) AMERICAN CYANAMID CO.

PA

XX Chaleff RS, Hand JM, Singh BK;  
 XX WPI; 1992-218438/27.  
 XX Acetohydroxy acid synthase enzyme deletion mutants - encoded by  
 XX nucleic acid sequences which can confer herbicide resistance to  
 XX plants  
 XX Claim 4; Page 20; 37pp; English.  
 XX The sequence is that of Ser653 deleted acetohydroxy acid synthase  
 CC (AHAS) which is herbicide resistant. Transgenic plants may be  
 CC produced which contain the modified gene and produce the Ser653  
 CC deleted AHAS in the presence of an inhibitory amt. of herbicide.  
 CC The gene can thus be used to provide crop plants with resistance  
 CC to herbicides such as imidazolinones, triazolopyrimidines and  
 CC sulphonylureas. See also AAR4798-R24801 and AAR28609-R28624.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 669 AA;

Query Match 99.3%; Score 3425.5; DB 13; Length 669;

Best Local Similarity 99.7%; Pred. No. 2.3e-276;

Matches 668; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAAATTTTSSSSISFKPSSSKSPLFISFSLPNSKSSSSRRRGKSSSPS 60

Db 1 MAAATTTTSSSSISFKPSSSKSPLFISFSLPNSKSSSSRRRGKSSSPS 60

QY 61 SISAVLNTNTNTTSPSTKPTETISRFAPDQPRKGADILVEALERQGVETVFAYPG 120

Db 61 SISAVLNTNTNTTSPSTKPTETISRFAPDQPRKGADILVEALERQGVETVFAYPG 120

QY 121 GASMEIHOALTTRSSISRNVLPRHQGVFAAGYARSSKPGICGICATSPGATNLVSGLA 180

Db 121 GASMEIHOALTTRSSISRNVLPRHQGVFAAGYARSSKPGICGICATSPGATNLVSGLA 180

QY 181 DALLDSVPLVAITGVQPRRMIGTDAFOETPIVEVTRSTIKENYLVMDVEDIPRIIEBAFF 240

Db 181 DALLDSVPLVAITGVQPRRMIGTDAFOETPIVEVTRSTIKENYLVMDVEDIPRIIEBAFF 240

QY 241 LATSGRPGVLVDVFKDIOQOLAI PNWQAMRLPGYMSRMKPPEDSHLEQIVRLISESK 300

Db 241 LATSGRPGVLVDVFKDIOQOLAI PNWQAMRLPGYMSRMKPPEDSHLEQIVRLISESK 300

QY 301 KPVLYVGGGCLNSDELGRFVELTGIPVASTLMLGSGYPCDDDELSTHMLGMEGTVYANYA 360

Db 301 KPVLYVGGGCLNSDELGRFVELTGIPVASTLMLGSGYPCDDDELSTHMLGMEGTVYANYA 360

QY 361 VEHSDLLAFGVFRDRTVTKLEAFASRAKIVHIDISAEIGKNTPHVSGDVYKALQ 420

Db 361 VEHSDLLAFGVFRDRTVTKLEAFASRAKIVHIDISAEIGKNTPHVSGDVYKALQ 420

QY 421 GNMKVLNRAEELKLDGFWNRNELNVQKFPPLSPKTFGEAIPPOYAIKVLDELTDGKAI 480

Db 421 GNMKVLNRAEELKLDGFWNRNELNVQKFPPLSPKTFGEAIPPOYAIKVLDELTDGKAI 480

QY 481 ISTGVGHQWMAAOFYNYKKPRLNNOHLMGMWOWEDRFYKANRAHTFLGDPACDEIFPN 600

Db 481 ISTGVGHQWMAAOFYNYKKPRLNNOHLMGMWOWEDRFYKANRAHTFLGDPACDEIFPN 600

QY 601 MLLFAAACGIPAAVTVTKADIREALQTMLDTPGTYLLDVI CPHQEHVLPMPISGTFENDV 660

Db 601 MLLFAAACGIPAAVTVTKADIREALQTMLDTPGTYLLDVI CPHQEHVLPMPISGTFENDV 660

QY 661 ITGEGRIKY 670

Db 660 ITGEGRIKY 669





QY 601 MLLFAACGIPAAVTKKADLREAIQTMLDTGPGYLLDVICPHQEHVLPMPNGGTFNDV 660  
 DB 600 MLLFAACGIPAAVTKKADLREAIQTMLDTGPGYLLDVICPHQEHVLPMPNGGTFNDV 659  
 QY 661 ITEGDGRIKY 670  
 DB 660 ITEGDGRIKY 669

RESULT 15  
 AAR28620  
 ID AAR28620 standard; Protein; 669 AA.  
 XX AC  
 XX AAR28620;  
 XX  
 XX 25-MAR-2003 (updated)  
 XX 11-DEC-1992 (first entry)  
 XX  
 XX Lys256 deleted acetohydroxy acid synthase.  
 XX AHAS; herbicide resistance; plants; imidazolinones;  
 XX triazolopyrimidines; sulphonylureas.  
 XX Arabidopsis.thaliana.  
 XX OS  
 XX EP492113-A2.  
 XX  
 XX 01-JUL-1992.  
 XX  
 XX 12-NOV-1991; 91EP-0119254.  
 XX  
 XX 27-DEC-1990; 90US-0633210.  
 XX (AMCY ) AMERICAN CYANAMID CO.  
 XX PA  
 XX Chaleff RS, Hand JM, Singh BK;  
 XX WPI; 1992-218438/27.  
 XX  
 XX Aceto:hydroxy acid synthase enzyme deletion mutants - encoded by  
 PT nucleic acid sequences which can confer herbicide resistance to  
 PT plants  
 XX PT  
 XX Claim 4; Page 20; 37pp; English.  
 XX  
 XX The sequence is that of Lys256 deleted acetohydroxy acid synthase  
 CC (AHAS) which is herbicide resistant. Transgenic plants may be  
 CC produced which contain the modified gene and produce the Lys256  
 CC deleted AHAS in the presence of an inhibitory amt. of herbicide.  
 CC The gene can thus be used to provide crop plants with resistance  
 CC to herbicides such as imidazolinones, triazolopyrimidines and  
 CC sulphonylureas. See also AAR24798-R24801 and AAR28609-R28624.  
 CC (Updated on 25-MAR-2003 to correct FN field.)  
 XX  
 XX Sequence 669 AA;  
 SQ

Query Match 99.2%; Score 3421.5; DB 13; Length 669;  
 Best Local Similarity 99.6%; Pred. No. 5e-276;  
 Matches 667; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 MAAATTTTSSSISGSKPSPSSKSPLPISRFSLPSPINPNKSSSSRRRGKSSSPS 60  
 DB 1 MAAATTTTSSSISGSKPSPSSKSPLPISRFSLPSPINPNKSSSSRRRGKSSSPS 60  
 QY 61 SISAVLNTNTTTPSPKTKPTEPFISRFAPDOPRKGADILVEALERQGVETVFAYPG 120  
 DB 61 SISAVLNTNTTTPSPKTKPTEPFISRFAPDOPRKGADILVEALERQGVETVFAYPG 120  
 QY 121 GASMEIHQALTRSSSRNVLPFRHQGGVFAAGYARSSGKPGICATSGPGATNVSGLA 180  
 DB 121 GASMEIHQALTRSSSRNVLPFRHQGGVFAAGYARSSGKPGICATSGPGATNVSGLA 180

QY 181 DALLDSVPLVAITGOVPRWIGTDAFOETPIVETBSITKKNYLVMVDVEDIPRIIEAFF 240  
 DB 181 DALLDSVPLVAITGOVPRWIGTDAFOETPIVETBSITKKNYLVMVDVEDIPRIIEAFF 240  
 QY 241 LATSGRPGVLDVDPKDIQQQLAIPNWEQAMRLPGYMSMPKPPEDSHLEQIVRLISESK 300  
 DB 241 LATSGRPGVLDVDP-DIQQQLAIPNWEQAMRLPGYMSMPKPPEDSHLEQIVRLISESK 299  
 QY 301 KPVLVGGGCLNSDELGRFVELTGI PVASTLMGLSGYPCDDLSLHMLGNHGTYYANYA 360  
 DB 300 KPVLVGGGCLNSDELGRFVELTGI PVASTLMGLSGYPCDDLSLHMLGNHGTYYANYA 359  
 QY 361 VEHSDLLAFGVRFDDRVVTGKLEAFASRAKI VHIIDISAEIGKNTPHVSVCGDVKLAIQ 420  
 DB 360 VEHSDLLAFGVRFDDRVVTGKLEAFASRAKI VHIIDISAEIGKNTPHVSVCGDVKLAIQ 419  
 QY 421 GNNKYLENRAEELKLDGFWRNELNVOKFPLSPKTFGEAIPPOYAIKVLDELTDGKAI 480  
 DB 420 GNNKYLENRAEELKLDGFWRNELNVOKFPLSPKTFGEAIPPOYAIKVLDELTDGKAI 479  
 QY 481 ISTGVGQHOMWAAQFYNNKKPQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDS 540  
 DB 480 ISTGVGQHOMWAAQFYNNKKPQWLSSGGLGAMGFLPAAIGASVANPDAIVVDIDGDS 539  
 QY 541 ETMNVQELATIRVENLPVKVLLANNCHLGMVQWEDRFYKANRAHTFLGDPAGEDEIFEN 600  
 DB 540 ETMNVQELATIRVENLPVKVLLANNCHLGMVQWEDRFYKANRAHTFLGDPAGEDEIFEN 599  
 QY 601 MLLFAACGIPAAVTKKADLREAIQTMLDTGPGYLLDVICPHQEHVLPMPNGGTFNDV 660  
 DB 600 MLLFAACGIPAAVTKKADLREAIQTMLDTGPGYLLDVICPHQEHVLPMPNGGTFNDV 659  
 QY 661 ITEGDGRIKY 670  
 DB 660 ITEGDGRIKY 669

Search completed: July 25, 2003, 10:47:12  
 Job time : 88 secs



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OM protein - protein search, using sw model

Run on: July 25, 2003, 10:46:18 ; Search time 31 Seconds  
(without alignments)  
914.460 Million cell updates/sec

Title: US-10-057-609B-3  
Perfect score: 3448  
Sequence: 1 MAAATTTTSSISFSTKP.....IPNGGTVDVTEGRIKY 670

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3448	100.0	670	1 US-08-363-208-2	Sequence 2, Appli
2	3448	100.0	670	2 US-09-137-478-2	Sequence 2, Appli
3	3437.5	99.7	671	2 US-08-426-125-8	Sequence 8, Appli
4	3437.5	99.7	671	2 US-08-455-355-8	Sequence 8, Appli
5	3437.5	99.7	671	4 US-09-367-512-7	Sequence 7, Appli
6	3017	87.5	652	2 US-08-426-125-9	Sequence 9, Appli
7	3017	87.5	652	2 US-08-455-355-9	Sequence 9, Appli
8	3017	87.5	652	4 US-09-367-512-8	Sequence 8, Appli
9	2683	77.8	664	2 US-08-426-125-7	Sequence 7, Appli
10	2683	77.8	664	2 US-08-455-355-7	Sequence 7, Appli
11	2683	77.8	664	4 US-09-367-512-6	Sequence 6, Appli
12	2671	77.5	648	1 US-08-321-356-4	Sequence 4, Appli
13	2666.5	77.3	667	2 US-08-426-125-6	Sequence 6, Appli
14	2666.5	77.3	667	2 US-08-455-355-6	Sequence 6, Appli
15	2666.5	77.3	667	4 US-09-367-512-5	Sequence 5, Appli
16	2650	76.9	648	1 US-08-321-356-2	Sequence 2, Appli
17	2611	75.7	637	2 US-08-426-125-10	Sequence 10, Appl
18	2611	75.7	637	2 US-08-455-355-10	Sequence 10, Appl
19	2611	75.7	637	4 US-09-367-512-9	Sequence 9, Appli
20	2348.5	68.1	638	2 US-08-426-125-5	Sequence 5, Appli
21	2348.5	68.1	638	2 US-08-455-355-5	Sequence 5, Appli
22	2348.5	68.1	638	4 US-09-367-512-4	Sequence 4, Appli
23	2338	67.8	638	2 US-08-426-125-4	Sequence 4, Appli
24	2338	67.8	638	2 US-08-455-355-4	Sequence 4, Appli
25	2338	67.8	638	4 US-09-367-512-3	Sequence 3, Appli
26	2334.5	67.7	599	2 US-08-426-125-3	Sequence 3, Appli
27	2334.5	67.7	599	2 US-08-455-355-3	Sequence 3, Appli

28	2329.5	67.6	599	2 US-08-426-125-1	Sequence 1, Appli
29	2329.5	67.6	599	2 US-08-455-355-1	Sequence 1, Appli
30	2329.5	67.6	599	4 US-09-367-512-1	Sequence 1, Appli
31	1239.5	35.9	548	2 US-08-452-075-3	Sequence 3, Appli
32	1239.5	35.9	548	3 US-09-231-061-2	Sequence 2, Appli
33	1239.5	35.9	556	4 US-09-011-762-7	Sequence 7, Appli
34	1224	34.6	337	6 5202251-1	Patent No. 5202251
35	1193	34.6	575	1 US-08-403-866-7	Sequence 7, Appli
36	1123	32.6	584	4 US-09-134-001C-3884	Sequence 3884, Ap
37	1118.5	32.4	580	4 US-09-252-991A-23699	Sequence 23699, A
38	1090	31.6	576	4 US-09-328-352-8068	Sequence 8068, Ap
39	694.5	20.1	622	4 US-09-252-991A-27587	Sequence 27587, A
40	641.5	18.6	579	4 US-09-252-991A-27970	Sequence 27970, A
41	617.5	17.9	624	4 US-09-252-991A-20490	Sequence 20490, A
42	561.5	16.3	554	4 US-09-134-001C-4402	Sequence 4402, Ap
43	545	15.8	581	4 US-09-107-532A-6835	Sequence 6835, Ap
44	538	15.6	807	4 US-09-252-991A-32992	Sequence 32992, A
45	524	15.2	586	4 US-09-134-001C-4456	Sequence 4456, Ap

## ALIGNMENTS

RESULT 1  
US-08-363-208-2  
; Sequence 2, Application US/08363208  
; Patent No. 5767366  
; GENERAL INFORMATION:  
; APPLICANT: Sathasivan, Kanagasabapathi  
; APPLICANT: Murai, No. 5767366Imoto  
; TITLE OF INVENTION: A Mutant Acetolactate Synthase Gene From  
; TITLE OF INVENTION: Arabidopsis Thaliana For Conferring Imidazolinone  
; TITLE OF INVENTION: Resistance To Crop Plants  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Llewellyn A. Proctor, Sr.  
; STREET: 11481 Sheraton Drive  
; CITY: Baton Rouge,  
; STATE: LA  
; COUNTRY: USA  
; ZIP: 70815  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/363,208  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/657,429  
; FILING DATE: 19-FEB-1991  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Proctor Sr., Llewellyn A.  
; REGISTRATION NUMBER: 20,152  
; REFERENCE/DOCKET NUMBER: 013911-001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (504)275-8689  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 670 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-363-208-2

Query Match 100.0%; Score 3448; DB 1; Length 670;  
Best Local Similarity 100.0%; Pred. No. 5e-307;  
Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAAATTTTSSISFSTKPSKSKPLTFRSLPFLPNKSSSSRRRIKSSPS 60

Db 1 MAAATTTTSSISFSSTKSPSSSKSLPISEFSLPSLNPNKSSSSRRGKSSSPS 60  
Qy 61 SISAVLNTNTTNTTTPSTKPTKPTFTFISRPADDPKRGADILVEALERQGVETVAYPG 120  
Db 61 SISAVLNTNTTNTTTPSTKPTKPTFTFISRPADDPKRGADILVEALERQGVETVAYPG 120  
Qy 121 GASMEIHOALTRSSSIRNVLPRIHQGVFAAGVARSKPGICATSPCATNLVSGLA 180  
Db 121 GASMEIHOALTRSSSIRNVLPRIHQGVFAAGVARSKPGICATSPCATNLVSGLA 180  
Qy 181 DALLDSVPLVAITGOVPRMIGTDAFOETPIVEVTRSTIKHNYLVMDVEDIPRIIEAFF 240  
Db 181 DALLDSVPLVAITGOVPRMIGTDAFOETPIVEVTRSTIKHNYLVMDVEDIPRIIEAFF 240  
Qy 241 LATSGRPGPVLVDVFKDIQQQLAIPNWEQAMLPQYMRMPKPPEDSHLEQIVRLISESK 300  
Db 241 LATSGRPGPVLVDVFKDIQQQLAIPNWEQAMLPQYMRMPKPPEDSHLEQIVRLISESK 300  
Qy 301 KPVLVYGGGCLNSSDELGRFVELTGIPVASTLMGLSGYPCCDDELSLHMLGMHGTVYANYA 360  
Db 301 KPVLVYGGGCLNSSDELGRFVELTGIPVASTLMGLSGYPCCDDELSLHMLGMHGTVYANYA 360  
Qy 361 VEHSDLLAFGVRFDDRTVTKLEAFASRAKIVHIDIDSARIGKNTKPHVSVCGDVKLALQ 420  
Db 361 VEHSDLLAFGVRFDDRTVTKLEAFASRAKIVHIDIDSARIGKNTKPHVSVCGDVKLALQ 420  
Qy 421 GMKVLNRAEELKLDGFWNRNELNVQKQPLSKFTFGAIPPOVAIKVDELTDGKAI 480  
Db 421 GMKVLNRAEELKLDGFWNRNELNVQKQPLSKFTFGAIPPOVAIKVDELTDGKAI 480  
Qy 481 ISTGVGQHMWAAQFYNYKKPQWLSGGLGANGFGLPAAIGASVANPDALVVIDDGGS 540  
Db 481 ISTGVGQHMWAAQFYNYKKPQWLSGGLGANGFGLPAAIGASVANPDALVVIDDGGS 540  
Qy 541 FIMNVQELATIRVENLPVKVLLNNOHLGMWQWEDRFYKANRAHTFLGDPQAQDEIFPN 600  
Db 541 FIMNVQELATIRVENLPVKVLLNNOHLGMWQWEDRFYKANRAHTFLGDPQAQDEIFPN 600  
Qy 601 MLLFAAACGIPAAVTKKADLREALIQTMLDTPGVLDDVCPHQEHVLPMPNGTNDV 660  
Db 601 MLLFAAACGIPAAVTKKADLREALIQTMLDTPGVLDDVCPHQEHVLPMPNGTNDV 660  
Qy 661 ITEGDRIRKY 670  
Db 661 ITEGDRIRKY 670

RESULT 2

US-09-137-478-2  
; Sequence 2, Application US/09137478  
; Patent No. 6225105  
; GENERAL INFORMATION:  
; APPLICANT: Sathasivan, Kanagasabapathi  
; APPLICANT: Murai, No. 6225105imoto  
; TITLE OF INVENTION: A Mutant Acetolactate Synthase Gene From Arabidopsis Thaliana For Conferring Imidazolinone Resistance To Crop Plants  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Llewellyn A. Proctor, Sr.  
; STREET: 11481 Sheraton Drive  
; CITY: Baton Rouge,  
; STATE: LA  
; COUNTRY: USA  
; ZIP: 70815  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/137,478

; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/657,429  
; FILING DATE: 19-FEB-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Proctor Sr., Llewellyn A.  
; REGISTRATION NUMBER: 20,152  
; REFERENCE/DOCKET NUMBER: 013911-001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (504)275-8689  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 670 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-137-478-2  
Query Match 100.0%; Score 3448; DB 3; Length 670;  
Best Local Similarity 100.0%; Pred. No. 5e-307;  
Matches 670; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAAATTTTSSISFSSTKSPSSSKSLPISEFSLPSLNPNKSSSSRRGKSSSPS 60  
Db 1 MAAATTTTSSISFSSTKSPSSSKSLPISEFSLPSLNPNKSSSSRRGKSSSPS 60  
Qy 61 SISAVLNTNTTNTTTPSTKPTKPTFTFISRPADDPKRGADILVEALERQGVETVAYPG 120  
Db 61 SISAVLNTNTTNTTTPSTKPTKPTFTFISRPADDPKRGADILVEALERQGVETVAYPG 120  
Qy 121 GASMEIHOALTRSSSIRNVLPRIHQGVFAAGVARSKPGICATSPCATNLVSGLA 180  
Db 121 GASMEIHOALTRSSSIRNVLPRIHQGVFAAGVARSKPGICATSPCATNLVSGLA 180  
Qy 181 DALLDSVPLVAITGOVPRMIGTDAFOETPIVEVTRSTIKHNYLVMDVEDIPRIIEAFF 240  
Db 181 DALLDSVPLVAITGOVPRMIGTDAFOETPIVEVTRSTIKHNYLVMDVEDIPRIIEAFF 240  
Qy 241 LATSGRPGPVLVDVFKDIQQQLAIPNWEQAMLPQYMRMPKPPEDSHLEQIVRLISESK 300  
Db 241 LATSGRPGPVLVDVFKDIQQQLAIPNWEQAMLPQYMRMPKPPEDSHLEQIVRLISESK 300  
Qy 301 KPVLVYGGGCLNSSDELGRFVELTGIPVASTLMGLSGYPCCDDELSLHMLGMHGTVYANYA 360  
Db 301 KPVLVYGGGCLNSSDELGRFVELTGIPVASTLMGLSGYPCCDDELSLHMLGMHGTVYANYA 360  
Qy 361 VEHSDLLAFGVRFDDRTVTKLEAFASRAKIVHIDIDSARIGKNTKPHVSVCGDVKLALQ 420  
Db 361 VEHSDLLAFGVRFDDRTVTKLEAFASRAKIVHIDIDSARIGKNTKPHVSVCGDVKLALQ 420  
Qy 421 GMKVLNRAEELKLDGFWNRNELNVQKQPLSKFTFGAIPPOVAIKVDELTDGKAI 480  
Db 421 GMKVLNRAEELKLDGFWNRNELNVQKQPLSKFTFGAIPPOVAIKVDELTDGKAI 480  
Qy 481 ISTGVGQHMWAAQFYNYKKPQWLSGGLGANGFGLPAAIGASVANPDALVVIDDGGS 540  
Db 481 ISTGVGQHMWAAQFYNYKKPQWLSGGLGANGFGLPAAIGASVANPDALVVIDDGGS 540  
Qy 541 FIMNVQELATIRVENLPVKVLLNNOHLGMWQWEDRFYKANRAHTFLGDPQAQDEIFPN 600  
Db 541 FIMNVQELATIRVENLPVKVLLNNOHLGMWQWEDRFYKANRAHTFLGDPQAQDEIFPN 600  
Qy 601 MLLFAAACGIPAAVTKKADLREALIQTMLDTPGVLDDVCPHQEHVLPMPNGTNDV 660  
Db 601 MLLFAAACGIPAAVTKKADLREALIQTMLDTPGVLDDVCPHQEHVLPMPNGTNDV 660  
Qy 661 ITEGDRIRKY 670  
Db 661 ITEGDRIRKY 670

RESULT 3





US-08-455-355-8

Query Match 99.7%; Score 3437.5; DB 2; Length 671;  
 Best Local Similarity 99.9%; Pred. No. 4.6e-306;  
 Matches 670; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAAATTTTSSISFSTKSPSSSKSPPLISRFSLPFLSNPNKSSSSRRRGKSSSPS 60  
 DB 1 MAAATTTTSSISFSTKSPSSSKSPPLISRFSLPFLSNPNKSSSSRRRGKSSSPS 60

QY 61 SISAVLNTTNTTTPSPKTPETFIISRFAPDQPRKADILVLEALRQGVETVFAYPG 120  
 DB 61 SISAVLNTTNTTTPSPKTPETFIISRFAPDQPRKADILVLEALRQGVETVFAYPG 120

QY 121 GASMEIHOALTRSSIRNVLPREHOGGVFAAGYARSSGKPGICATSPGATNLVSGLA 180  
 DB 121 GASMEIHOALTRSSIRNVLPREHOGGVFAAGYARSSGKPGICATSPGATNLVSGLA 180

QY 181 DALLDSVPLVAITQGVPRRMIGTDAFOETPIVEVTRSIKHNLYVMDVEDIPRIIEA 240  
 DB 181 DALLDSVPLVAITQGVPRRMIGTDAFOETPIVEVTRSIKHNLYVMDVEDIPRIIEA 240

QY 241 LATSGRPGVLDVDPKDIQQOLAI PNWEOAMELPGYMSRMKPPEDSHLEQIVELISESK 300  
 DB 241 LATSGRPGVLDVDPKDIQQOLAI PNWEOAMELPGYMSRMKPPEDSHLEQIVELISESK 300

QY 301 KPVLVYGGGCLNSDELGRFVELTGPVASTLMGLGSPCDDLSLHMLGMHGTVYANYA 360  
 DB 301 KPVLVYGGGCLNSDELGRFVELTGPVASTLMGLGSPCDDLSLHMLGMHGTVYANYA 360

QY 361 VEHSDDLALAFGRVDRVTGKLEAFASRAKIVHIDISAEIGKNTKPHVSVCGVKALQ 420  
 DB 361 VEHSDDLALAFGRVDRVTGKLEAFASRAKIVHIDISAEIGKNTKPHVSVCGVKALQ 420

QY 421 GNMKVLNRAEELKLDGFWNRNENLVOKKPLSFKTGFEAIPPOVAIKVLDELTDGKAI 480  
 DB 421 GNMKVLNRAEELKLDGFWNRNENLVOKKPLSFKTGFEAIPPOVAIKVLDELTDGKAI 480

QY 481 ISTGVGQHOVMAAOFYNYKPP-ROWLSSGGLGAMGFLPAAGASVANPDAIVDDIDGG 539  
 DB 481 ISTGVGQHOVMAAOFYNYKPP-ROWLSSGGLGAMGFLPAAGASVANPDAIVDDIDGG 540

QY 540 SFTMNVQELATIRVENLPVKVLLNNQHLGNVMOQWEDRFYKANRAHTFLGDPQAEDEIFP 599  
 DB 541 SFTMNVQELATIRVENLPVKVLLNNQHLGNVMOQWEDRFYKANRAHTFLGDPQAEDEIFP 600

QY 600 NMLLFAAACGIPAAKVTCKADLREAIQTMLDTPGYLLDVI CPHOEHVLPMPNGGTND 659  
 DB 601 NMLLFAAACGIPAAKVTCKADLREAIQTMLDTPGYLLDVI CPHOEHVLPMPNGGTND 660

QY 660 VITEGDGRIKY 670  
 DB 661 VITEGDGRIKY 671

## RESULT 5

US-09-367-512-7  
 ; Sequence 7, Application US/09367512  
 ; Patent No. 6576455  
 ; GENERAL INFORMATION:  
 ; APPLICANT: American Cyanamid Company  
 ; APPLICANT: Kakeruda, Genichi  
 ; APPLICANT: Ott, Karl-Heinz  
 ; APPLICANT: Kwagh, Jae-Gyu  
 ; APPLICANT: Stockton, Gerald W.  
 ; TITLE OF INVENTION: Structure-based Designed Herbicide Resistant  
 ; FILE REFERENCE: 3489/1A674-US3  
 ; CURRENT APPLICATION NUMBER: US/09367,512  
 ; CURRENT FILING DATE: 2000-08-17  
 ; PRIOR APPLICATION NUMBER: 08/426,125  
 ; PRIOR FILING DATE: 1995-04-20  
 ; PRIOR APPLICATION NUMBER: 08/455,355

; PRIOR FILING DATE: 1995-05-31  
 ; PRIOR APPLICATION NUMBER: PCT/US96/05782  
 ; PRIOR FILING DATE: 1996-04-19  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 671  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-09-367-512-7

Query Match 99.7%; Score 3437.5; DB 4; Length 671;  
 Best Local Similarity 99.9%; Pred. No. 4.6e-306;  
 Matches 670; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MAAATTTTSSISFSTKSPSSSKSPPLISRFSLPFLSNPNKSSSSRRRGKSSSPS 60  
 DB 1 MAAATTTTSSISFSTKSPSSSKSPPLISRFSLPFLSNPNKSSSSRRRGKSSSPS 60

QY 61 SISAVLNTTNTTTPSPKTPETFIISRFAPDQPRKADILVLEALRQGVETVFAYPG 120  
 DB 61 SISAVLNTTNTTTPSPKTPETFIISRFAPDQPRKADILVLEALRQGVETVFAYPG 120

QY 121 GASMEIHOALTRSSIRNVLPREHOGGVFAAGYARSSGKPGICATSPGATNLVSGLA 180  
 DB 121 GASMEIHOALTRSSIRNVLPREHOGGVFAAGYARSSGKPGICATSPGATNLVSGLA 180

QY 181 DALLDSVPLVAITQGVPRRMIGTDAFOETPIVEVTRSIKHNLYVMDVEDIPRIIEA 240  
 DB 181 DALLDSVPLVAITQGVPRRMIGTDAFOETPIVEVTRSIKHNLYVMDVEDIPRIIEA 240

QY 241 LATSGRPGVLDVDPKDIQQOLAI PNWEOAMELPGYMSRMKPPEDSHLEQIVELISESK 300  
 DB 241 LATSGRPGVLDVDPKDIQQOLAI PNWEOAMELPGYMSRMKPPEDSHLEQIVELISESK 300

QY 301 KPVLVYGGGCLNSDELGRFVELTGPVASTLMGLGSPCDDLSLHMLGMHGTVYANYA 360  
 DB 301 KPVLVYGGGCLNSDELGRFVELTGPVASTLMGLGSPCDDLSLHMLGMHGTVYANYA 360

QY 361 VEHSDDLALAFGRVDRVTGKLEAFASRAKIVHIDISAEIGKNTKPHVSVCGVKALQ 420  
 DB 361 VEHSDDLALAFGRVDRVTGKLEAFASRAKIVHIDISAEIGKNTKPHVSVCGVKALQ 420

QY 421 GNMKVLNRAEELKLDGFWNRNENLVOKKPLSFKTGFEAIPPOVAIKVLDELTDGKAI 480  
 DB 421 GNMKVLNRAEELKLDGFWNRNENLVOKKPLSFKTGFEAIPPOVAIKVLDELTDGKAI 480

QY 481 ISTGVGQHOVMAAOFYNYKPP-ROWLSSGGLGAMGFLPAAGASVANPDAIVDDIDGG 539  
 DB 481 ISTGVGQHOVMAAOFYNYKPP-ROWLSSGGLGAMGFLPAAGASVANPDAIVDDIDGG 540

QY 540 SFTMNVQELATIRVENLPVKVLLNNQHLGNVMOQWEDRFYKANRAHTFLGDPQAEDEIFP 599  
 DB 541 SFTMNVQELATIRVENLPVKVLLNNQHLGNVMOQWEDRFYKANRAHTFLGDPQAEDEIFP 600

QY 600 NMLLFAAACGIPAAKVTCKADLREAIQTMLDTPGYLLDVI CPHOEHVLPMPNGGTND 659  
 DB 601 NMLLFAAACGIPAAKVTCKADLREAIQTMLDTPGYLLDVI CPHOEHVLPMPNGGTND 660

QY 660 VITEGDGRIKY 670  
 DB 661 VITEGDGRIKY 671

## RESULT 6

US-08-426-125-9  
 ; Sequence 9, Application US/08426125  
 ; Patent No. 5853973  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kakeruda, Genichi  
 ; APPLICANT: Ott, Karl-Heinz  
 ; APPLICANT: Kwagh, Jae-Gyu  
 ; APPLICANT: Stockton, Gerald W.

;; TITLE OF INVENTION: Structure-Based Designed Herbicide  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Darby & Darby  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10022-7513  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/426,125  
;; FILING DATE: 20-APR-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Robinson, Joseph  
;; REGISTRATION NUMBER: 33,448  
;; REFERENCE/DOCKET NUMBER: 0646/0A674  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212)-527-7783  
;; TELEFAX: (212)-753-6237  
;; TELEX: 236687  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 652 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHEICAL: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Brassica napus  
;; US-08-426-125-9

Query Match 87.5%; Score 3017; DB 2; Length 652;  
Best Local Similarity 88.4%; Pred. No. 1.5e-267;  
Matches 592; Conservative 29; Mismatches 31; Indels 18; Gaps 4;  
  
QY 1 MAATTTTSSISFSTKPSGSSKPLFISRFSLPSPNPNKSSSSRRRGKSSSPS 60  
DB 1 MAAA---TSSSFISLTAKP---SSKSPLFISRFSLPSPNPNKSSSSRRRGKSSSPS 46  
  
QY 61 SISAVLNTNTTTPSPKTKDETFISRPADQPRKGADILVEALEREQGVETVAYPG 120  
DB 47 AISAVLNSPVNV---APEKTKIKTFISRYAPDPRKGADILVEALEREQGVETVAYPG 102  
  
QY 121 GASMEIHOALTSRSSIRNVLPRHQGGVFAAGYARSSGKFGICATSGFGATNLVSGLA 180  
DB 103 GASMEIHOALTSRSSIRNVLPRHQGGVFAAGYARSSGKFGICATSGFGATNLVSGLA 162  
  
QY 181 DALDLSVELVAITGVPMRTGDAQOETPIVETVRSITKHNYLWMDVEDIPRIIEAEP 240  
DB 163 DAMDLSVELVAITGVPMRTGDAQOETPIVETVRSITKHNYLWMDVEDIPRIIEAEP 222  
  
QY 241 LATSGRPGVLVDVFKDIQQQLAIPNWDQPMELPGYNSRLPQPEVSLGQIVRLISESK 300  
DB 223 LATSGRPGVLVDVFKDIQQQLAIPNWDQPMELPGYNSRLPQPEVSLGQIVRLISESK 282  
  
QY 301 KPVLYVGGGLNSDELGRFVELIGIPVASTLMGLGSPCDDELISLHMGEGITVANYA 360  
DB 283 KPVLYVGGGLNSDELGRFVELIGIPVASTLMGLGSPCDDELISLHMGEGITVANYA 342  
  
QY 361 VEHSDLLAFGVRFDDRTVTKLEAFASRAKIVHIDISAEIGKKNKPHVSCGVKLAIQ 420  
DB 343 VEHSDLLAFGVRFDDRTVTKLEAFASRAKIVHIDISAEIGKKNKPHVSCGVKLAIQ 402  
  
QY 421 GNNKVLNRAEELKLDGFWNRSELSEQKQKFPPLSKFTGFAIPPOYAIQVDELDTQKAI 480

DB 403 GNNKVLNRAEELKLDGFWNRSELSEQKQKFPPLSKFTGFAIPPOYAIQVDELDTQKAI 462  
QY 481 ISTGVGOHWMAQFYNKKPRQWLSSGGLGAMGFGLPAAIGASVANPDALVVDIDGGS 540  
DB 463 ISTGVGOHWMAQFYNKKPRQWLSSGGLGAMGFGLPAAIGASVANPDALVVDIDGGS 522  
QY 541 FIMNVOELATIRVENLFPVKVLLNNNOHLGVMQWEDRFYKANRAHTFLGDPQEDHIFN 600  
DB 523 FIMNVOELATIRVENLFPVKVLLNNNOHLGVMQWEDRFYKANRAHTFLGDPQEDHIFN 582  
QY 601 MLFPAACGIPARVTKKADAREATQMLDTPGPLYLDVLCPOHSHVLMIPNGETENDV 660  
DB 583 MLQFAGACGIPARVTKKAGELREALQTMLDTPGPLYLDVLCPOHSHVLMIPNGETENDV 642  
QY 661 ITEGDGRYK 670  
DB 643 ITEGDGRYK 652

## RESULT 7

US-08-455-355-9  
; Sequence 9, Application US/08455355  
; Patent No. 5928937  
; GENERAL INFORMATION:  
; APPLICANT: Kakefuda, Genichi  
; APPLICANT: Ott, Karl-Heinz  
; APPLICANT: Kwagh, Jae-Gyu  
; APPLICANT: Stockton, Gerald W.  
; TITLE OF INVENTION: Structure-Based Designed Herbicide  
; TITLE OF INVENTION: Resistant Products  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022-7513  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,355  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robinson, Joseph  
; REGISTRATION NUMBER: 33,448  
; REFERENCE/DOCKET NUMBER: 0646/1A674-US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)-527-7783  
; TELEFAX: (212)-753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 652 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Brassica napus  
; US-08-455-355-9

Query Match 87.5%; Score 3017; DB 2; Length 652;  
Best Local Similarity 88.4%; Pred. No. 1.5e-267;  
Matches 592; Conservative 29; Mismatches 31; Indels 18; Gaps 4;  
  
QY 1 MAATTTTSSISFSTKPSGSSKPLFISRFSLPSPNPNKSSSSRRRGKSSSPS 60

[illegible]

RESULT 9  
US-08-426-125-7  
; Sequence 7, Application US/08426125  
; Patent No. 5853973  
; GENERAL INFORMATION:  
; APPLICANT: Kakafuda, Genichi  
; APPLICANT: Ott, Karl-Heinz  
; APPLICANT: Kwagh, Jae-Gyu  
; APPLICANT: Stockton, Gerald W.  
; TITLE OF INVENTION: Structure-Based Designed Herbicide  
; TITLE OF INVENTION: Resistant Products  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York

COUNTRY: USA  
ZIP: 10022-7513  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/426,125  
FILING DATE: 20-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robinson, Joseph  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 0646/0A674  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)-527-7783  
TELEFAX: (212)-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 664 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-426-125-7

Query Match 77.8%; Score 2683; DB 2; Length 664;  
Best Local Similarity 76.8%; Pred. No. 6.2e-237;  
Matches 523; Conservative 58; Mismatches 72; Indels 28; Gaps 4;  
QY 1 MAAATTTTSSISFSTKPSKSSKSPISRFSLPSLNPKSS-----SSS 49  
Db 1 MAAA-----AAAPSPFSKTLSSSSKSTLLPRSTFPFPHPHKTPPPPLHTPTHISQ 56  
QY 50 RRGKXSSPSSISAVLNTTNTVTPSPKPTKPTFISRPAPDPRKADILVEALER 109  
Db 57 RRR-----FTISNVISTQKVSET-----QKAETFSRFPAPDEPRKGSVLVEALER 103  
QY 110 QGVETVPYVPGASMEHQALTRSSSIIRNVLPRHOGGVFAAGYARSGKPGCIATSG 169  
Db 104 EGVTDVFAIPGGASMEHQALTRSSSIIRNVLPRHOGGVFAAGYARATGFGVCIATSG 163  
QY 170 PGATNLVSGDALDLSVPLVAITGVQVPRRMIGTDAFOETPIVEVTRSTIKHNLVMDVE 229  
Db 164 PGATNLVSGDALDLSVPLVAITGVQVPRRMIGTDAFOETPIVEVTRSTIKHNLVMDVE 223  
QY 230 DIPRIIEAFLATSGRRGPVLVDVKDIOOOLAIIPNWEQAMLPQYMSRMPKPEDSHL 289  
Db 224 DIPRVVREAFFLARGRPVPLVDVKDIOOOLVLPDWDQPMRLPGYMSRLPKPNEMLL 283  
QY 290 EQIVRLISSEKPVLYVGGGLNSSLDELGRFVELTGPVASTLWGLSGYPCDDELISLML 349  
Db 284 EQIVRLISSEKPVLYVGGGLNSSLDELGRFVELTGPVASTLWGLSGYPCDDELISLML 343  
QY 350 GMGTIVANYAEHSDLLAFGRFDRVTGKLEAPASRAKIVHIDISAEIGKNTKPHY 409  
Db 344 GMGTIVANYAVDSDDLAFGRFDRVTGKLEAPASRAKIVHIDISAEIGKNTKPHY 403  
QY 410 SVCDVKALQGMNKVLENRAEELKLDGFWNRNELNVOKOFLPSFKTEGRAIPPOVAIK 469  
Db 404 SICADIKALQGNLSLESKEGLKLDPSAWOEQLTVQKYKYPINLKTFGDALPPOVAIK 463  
QY 470 VLDELTDGKALISTGVQHOWAAQFYNYKPKROWLSSGGLGAMGFLPAATGASVANPD 529  
Db 464 VLDELTDGKALISTGVQHOWAAQFYNYKPKROWLSSGGLGAMGFLPAATGASVANPD 523  
QY 530 AIVVDIDGSGSTFMMVQELATIRVENLPVKLLNNQHLGNVQWEDREYKANTHTFLG 589  
Db 524 EVVVDIDGSGSTFMMVQELATIRVENLPVKLLNNQHLGNVQWEDREYKANTHTFLG 583  
QY 590 DPAQDEDEIFFNMLFAACGIPAAVTRTKKADLREAIOITMLDTPGPYLLDVIQFQEHVLP 649

Db 584 NPSNEARLFFNNLKEAFACGVPAARVTHRDDLRAAIKMLDTPGYPYLLDVIQFQEHVLP 643  
QY 650 MIPNGGTNDVITEGDRIKY 670  
Db 644 MIPSGGAFKDVITEGDRSSY 664  
RESULT 10  
US-08-455-355-7  
Sequence 7; Application US/08455355  
Patent No. 5928937  
GENERAL INFORMATION:  
APPLICANT: Kakefuda, Genichi  
APPLICANT: Ott, Karl-Heinz  
APPLICANT: Kwagh, Jae-Gyu  
APPLICANT: Stockton, Gerald W.  
TITLE OF INVENTION: Structure-Based Designed Herbicide  
TITLE OF INVENTION: Resistant Products  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022-7513  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,355  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robinson, Joseph  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 0646/1A674-US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)-527-7783  
TELEFAX: (212)-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 664 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-455-355-7

Query Match 77.8%; Score 2683; DB 2; Length 664;  
Best Local Similarity 76.8%; Pred. No. 6.2e-237;  
Matches 523; Conservative 58; Mismatches 72; Indels 28; Gaps 4;  
QY 1 MAAATTTTSSISFSTKPSKSSKSPISRFSLPSLNPKSS-----SSS 49  
Db 1 MAAA-----AAAPSPFSKTLSSSSKSTLLPRSTFPFPHPHKTPPPPLHTPTHISQ 56  
QY 50 RRGKXSSPSSISAVLNTTNTVTPSPKPTKPTFISRPAPDPRKADILVEALER 109  
Db 57 RRR-----FTISNVISTQKVSET-----QKAETFSRFPAPDEPRKGSVLVEALER 103  
QY 110 QGVETVPYVPGASMEHQALTRSSSIIRNVLPRHOGGVFAAGYARSGKPGCIATSG 169  
Db 104 EGVTDVFAIPGGASMEHQALTRSSSIIRNVLPRHOGGVFAAGYARATGFGVCIATSG 163  
QY 170 PGATNLVSGDALDLSVPLVAITGVQVPRRMIGTDAFOETPIVEVTRSTIKHNLVMDVE 229  
Db 164 PGATNLVSGDALDLSVPLVAITGVQVPRRMIGTDAFOETPIVEVTRSTIKHNLVMDVE 223



TELEPHONE: (415)354-3588  
TELEFAX: (415)857-1125  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: Protein  
US-08-321-356-4

Query Match 77.5%; Score 2671; DB 1; Length 648;  
Best Local Similarity 77.6%; Pred. No. 7.5e-236;  
Matches 521; Conservative 56; Mismatches 70; Indels 24; Gaps 6;

QY 1 MAAATTTTSSISFSTKPSKSPKPLISFSLPSPKSSSSRRRGKSSFS 60  
DB 1 MAAIPIHNP-----SITKPS-SSSPRPTFLARETFIT-----STSHKRR-----L 42  
QY 61 SISAVL-NTTNVITTPSKPKTPETISRFAPDQPKGADILVEALERQVETVFAYP 119  
DB 43 HSNVLSDEKTTIHSPLPK-----SFISYAPDQPKGADILVEALERQVETVFAYP 97  
QY 120 GGASMEIHOALTRSSIRNVLPRHEQGVFAAGYARSSGKPGICATSGPGATNLVSG 179  
DB 98 GGASMEIHOALTRSTIRNVLPRHEQGVFAAGYARSSGKPGICATSGPGATNLVSG 157  
QY 180 ADALDSDVLAITGOVPRMIGTDAFOETPIVETRSITKYNILVMDVEDIPRIIEAP 239  
DB 158 ADALDSDVLAITGOVPRMIGTDAFOETPIVETRSITKYNILVMDVEDIPRIIEAP 217  
QY 240 FLATSGRGPVLVDVDPKIQOOLAIIPNWEQAMLPVGMSPKPPEDSHLOIVRLIS 299  
DB 218 YLASSGRGPVLVDVDPKIQOOLAIIPNWEQAMLPVGMSPKPPEDSHLOIVRLIS 277  
QY 300 KQVLYVGGGCLNSDELGRFVELTGIPVASTLKGISYPCDDDELHMLGMGTGVANY 359  
DB 278 KQVLYVGGGCLNSDELGRFVELTGIPVASTLKGISYPCDDDELHMLGMGTGVANY 337  
QY 360 AVEHSDALLARGVDFDRVTGKLEAFASRAKIVHIDSDAEIGKNTPHVSVGDKVLA 419  
DB 338 AVDSKDLLARGVDFDRVTGKLEAFASRAKIVHIDSDAEIGKNTPHVSVGDKVLA 397  
QY 420 QGKVKLENRAELKLDGFWNRLNVQKPLSPFTKGEAIPPOYAIQVLDLTGKA 479  
DB 398 QGKVKLENRAELKLDGFWNRLNVQKPLSPFTKGEAIPPOYAIQVLDLTGKA 457  
QY 480 IISTGVGQHWAAQFYNYKKPROMLSSGGLGANGELPAATGASVANPDVVDIDGG 539  
DB 458 IISTGVGQHWAAQFYNYKKPROMLSSGGLGANGELPAATGASVANPDVVDIDGG 517  
QY 540 SFIMNVQSLATIRVENLPVKLLANNOHLMVMOWEDRFYKANRAHTPLGPAQDEIIP 599  
DB 518 SFIMNVQSLATIRVENLPVKLLANNOHLMVMOWEDRFYKANRAHTPLGPAQDEIIP 577  
QY 600 NMLFAACGTPAARVTKADIRRAITWMLDTPGPIVLDVCPHGHVLPIMPNGTFND 659  
DB 578 NMLFAACGTPAARVTKADIRRAITWMLDTPGPIVLDVCPHGHVLPIMPNGTFND 637  
QY 660 VITEGDRIKY 670  
DB 638 VITEGDRMKY 648

RESULT 13

US-08-426-125-6  
Sequence 6, Application US/09426125  
Patent No. 5853973  
GENERAL INFORMATION:  
APPLICANT: Kakeruda, Genichi  
APPLICANT: Ott, Karl-Heinz  
APPLICANT: Kwagh, Jae-Gyu  
APPLICANT: Stockton, Gerald W.

TITLE OF INVENTION: Structure-Based Designed Herbicide  
TITLE OF INVENTION: Resistant Products  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022-7513  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/426,125  
FILING DATE: 20-APR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robinson, Joseph  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 0646/OA674  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)-527-7783  
TELEFAX: (212)-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 667 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-426-125-6

Query Match 77.3%; Score 2666.5; DB 2; Length 667;  
Best Local Similarity 76.0%; Pred. No. 2e-235;  
Matches 519; Conservative 60; Mismatches 75; Indels 29; Gaps 4;

QY 1 MAAATTTTSSISFSTKPSKSPKPLISFSLPSPKSSSSRRRGKSSFS-----S 47  
DB 1 MAAA---APSPSSAFSKTSLSPSSSTSLPRSTPTFPFPHPHKTTTTPPLHLTHTHH 57  
QY 48 SRRRGKSSSPSSISAVLNTTNTTPTPTKPTETFSRPAQPKRGADILVEAL 107  
DB 58 SORRR-----FTISNVISTNQVSO-----EKTETFSRPAQPKRGADILVEAL 104  
QY 108 ERQGVETVPAYPGASMEIHOALTRSSIRNVLPRHEQGVFAAGYARSSGKPGICAT 167  
DB 105 ERQGVETVPAYPGASMEIHOALTRSSIRNVLPRHEQGVFAAGYARATGPGVCIAT 164  
QY 168 SGPATNLVSGDALDSDVLAITGOVPRMIGTDAFOETPIVETRSITKYNILVMD 227  
DB 165 SGPATNLVSGDALDSDVLAITGOVPRMIGTDAFOETPIVETRSITKYNILVMD 224  
QY 228 VBDIPRIIEAFFLATSGRPGFVLVDVDPKIQOOLAIIPNWEQAMLPVGMSPKPPEDS 287  
DB 225 VBDIPRIIEAFFLATSGRPGFVLVDVDPKIQOOLAIIPNWEQAMLPVGMSPKPPEDS 284  
QY 288 HLEQIVRLISESKPVLVYGGGCLNSDELGRFVELTGIPVASTLKGISYPCDDDEL 347  
DB 285 HLEQIVRLISESKPVLVYGGGCLNSDELGRFVELTGIPVASTLKGISYPCDDDEL 344  
QY 348 MLGMGTGVANYAVEHSDALLARGVDFDRVTGKLEAFASRAKIVHIDSDAEIGKNT 407  
DB 345 MLGMGTGVANYAVEHSDALLARGVDFDRVTGKLEAFASRAKIVHIDSDAEIGKNT 404  
QY 408 HVSVCQDVKALQGMKNVLENRAELKLDGFWNRLNVQKPLSPFTKGEAIPPOYA 467  
DB 405 HVSICADIKLALQGLNSILESKEGKLDGFWNRLNVQKPLSPFTKGEAIPPOYA 464



QY 468 IKVDELTDGKALISTGVGHQWMAAQFTYKPKROWLSSGGLGAMGFLPAALIGASVAN 527  
Db 465 IQVLDELTDGKALISTGVGHQWMAAQFTYKPKROWLSSGGLGAMGFLPAALIGAVGR 524  
QY 528 PDAIVVDIDGSGFTMNVQELATIRVENLPVKVLLINNOHLGNWQWEDRFYKANRAHTF 587  
Db 525 PDSVVVDIDGSGFTMNVQELATIRVENLPVKVLLINNOHLGNWQWEDRFYKANRAHTY 584  
QY 588 LSPDAQEDRIFPNMLLFAAACGIPAAARTVKKADLRRAIQTMLDTPGYPYLLDVICPHQEHV 647  
Db 585 LGNPSNEARIFPNMLKFAACGVPAAARTVTHRDDLRRAIQTMLDTPGYPYLLDVICPHQEHV 644  
QY 648 LPMIPNGGTFENDVITGEGRIKY 670  
Db 645 LPMIPSGGAFKDVITGEGRSSY 667

## RESULT 14

US-08-455-355-6  
; Sequence 6, Application US/08455355  
; Patent No. 5928937  
; GENERAL INFORMATION:  
; APPLICANT: Kakefuda, Genichi  
; APPLICANT: Ott, Karl-Heinz  
; APPLICANT: Kwagh, Jae-Gyu  
; APPLICANT: Stockton, Gerald W.  
; TITLE OF INVENTION: Structure-Based Designed Herbicide  
; TITLE OF INVENTION: Resistant Products  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022-7513  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/455,355  
; FILING DATE: 31-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robinson, Joseph  
; REGISTRATION NUMBER: 33,448  
; REFERENCE/DOCKET NUMBER: 0646/1A674-US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)-527-7783  
; TELEFAX: (212)-753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 667 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-455-355-6

Query Match 77.3%; Score 2666.5; DB 2; Length 667;  
Best Local Similarity 76.0%; Fred. No. 2e-235;  
Matches 519; Conservative 60; Mismatches 75; Indels 29; Gaps 4;  
QY 1 MAATTTTSSISFSTKSPSSKSLPLSRFSLPFLSNPKGS-----S 47  
Db 1 MAATTTTSSISFSTKSPSSKSLPLSRFSLPFLSNPKGS-----S 47  
QY 48 SSRRCIGKSSPSSISAVLNTTNTTTPSPKTKPKTPTISRFAPDQPRKGDILVEAL 107

Db 58 SQRRR-----FTISNVISTNQKVSQT-----EKTFTVSRFAPDQPRKGDILVEAL 104  
QY 108 EREGVETVFAVPGGASWEHQALFTSSIRNVLPRHEOGGVFAAGVARSQPGKICAT 167  
Db 105 EREGVETVFAVPGGASWEHQALFTSSIRNVLPRHEOGGVFAAGVARSQPGKICAT 164  
QY 168 SFGATNVLVGLDALLDSVPLVAITGVPRRMIGTDAFQETPIVETRSITKHNLVMD 227  
Db 165 SFGATNVLVGLDALLDSVPLVAITGVPRRMIGTDAFQETPIVETRSITKHNLVMD 224  
QY 228 VSDIPIITERAFPLATSGPGVPLVDPKDIQQOLAIWNQOAMELPGYMWKPKPDS 287  
Db 225 VSDIPIVREAFPLATSGPGVPLVDPKDIQQOLAIWNQOAMELPGYMWKPKPDS 284  
QY 288 HLEQIVRLISSEKPPVLYVGGGLNSSLDELGRFVELTGIPVASTLMGLSGYPCDDLSLH 347  
Db 285 HLEQIVRLISSEKPPVLYVGGGLNSSLDELGRFVELTGIPVASTLMGLSGYPCDDLSLH 344  
QY 348 MLGMEGTIVANYAVESDILLARGVREDRVTGKLARASRAKIVHIDISAEIGKNTK 407  
Db 345 MLGMEGTIVANYAVESDILLARGVREDRVTGKLARASRAKIVHIDISAEIGKNTK 404  
QY 408 HVSVCQDVKLALQGMNKVLENRAELKILDFGWRNELNVQKPPSLFKTFGEAIPPOVA 467  
Db 405 HVSICADIKLALQGLNLSILSEKGLKILDFSANRQELTKQVYKHPLEKTFGEAIPPOVA 464  
QY 468 IKVDELTDGKALISTGVGHQWMAAQFTYKPKROWLSSGGLGAMGFLPAALIGASVAN 527  
Db 465 IQVLDELTDGKALISTGVGHQWMAAQFTYKPKROWLSSGGLGAMGFLPAALIGAVGR 524  
QY 528 PDAIVVDIDGSGFTMNVQELATIRVENLPVKVLLINNOHLGNWQWEDRFYKANRAHTF 587  
Db 525 PDSVVVDIDGSGFTMNVQELATIRVENLPVKVLLINNOHLGNWQWEDRFYKANRAHTY 584  
QY 588 LSPDAQEDRIFPNMLLFAAACGIPAAARTVKKADLRRAIQTMLDTPGYPYLLDVICPHQEHV 647  
Db 585 LGNPSNEARIFPNMLKFAACGVPAAARTVTHRDDLRRAIQTMLDTPGYPYLLDVICPHQEHV 644  
QY 648 LPMIPNGGTFENDVITGEGRIKY 670  
Db 645 LPMIPSGGAFKDVITGEGRSSY 667

## RESULT 15

US-09-367-512-5  
; Sequence 5, Application US/09367512  
; Patent No. 6576455  
; GENERAL INFORMATION:  
; APPLICANT: American Cyanamid Company  
; APPLICANT: Kakefuda, Genichi  
; APPLICANT: Ott, Karl-Heinz  
; APPLICANT: Kwagh, Jae-Gyu  
; APPLICANT: Stockton, Gerald W.  
; TITLE OF INVENTION: Structure-Based Designed Herbicide Resistant  
; TITLE OF INVENTION: Products  
; FILE REFERENCE: 3489/1A674-US3  
; CURRENT APPLICATION NUMBER: US/09/367,512  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 08/426,125  
; PRIOR FILING DATE: 1995-04-20  
; PRIOR APPLICATION NUMBER: 08/455,355  
; PRIOR FILING DATE: 1995-05-31  
; PRIOR APPLICATION NUMBER: PCT/US96/05782  
; PRIOR FILING DATE: 1996-04-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 667  
; TYPE: PRT  
; ORGANISM: Tobacco  
US-09-367-512-5

Query Match 77.3%; Score 2666.5; DB 4; Length 667;



Search completed: July 25, 2003, 10:51:08  
Job time : 33 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: July 30, 2003, 08:16:31 ; Search time 5238 Seconds  
(without alignments)  
11167.743 Million cell updates/sec  
Title: US-10-057-609B-2  
Perfect score: 2010  
Sequence: 1 atggcggcggaacaacaac.....gagatggcggaataaacatc 2010

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.ov.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.pl.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sts.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.mu.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*  
29: em.vi.\*  
30: em.htg.hum.\*  
31: em.htg.inv.\*  
32: em.htg.other.\*  
33: em.htg.mus.\*  
34: em.htg.pln.\*  
35: em.htg.rod.\*  
36: em.htg.man.\*  
37: em.htg.vrt.\*  
38: em.sv.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2010	100.0	2365	6	AR148434
2	2010	100.0	2365	8	ATCGR12
3	2008.4	99.9	96679	8	AY048P19
4	2005.2	99.8	2263	8	AY042819
5	1978	98.4	2013	8	AY124092
6	1413.6	70.3	4724	8	BNHASYII
7	1398.8	69.6	3386	8	BNHASYII
8	1378.8	68.6	2019	8	BNHASYII
9	1345.2	66.9	1758	8	BNHASYII
10	1340.2	66.7	1758	8	BNHASYII
11	1338.6	66.6	1758	8	BNHASYII
12	1336.8	66.5	1758	8	BNHASYII
13	1336	66.5	1758	8	BNHASYII
14	1335.4	66.4	1758	8	BNHASYII
15	1329.4	66.1	1758	8	BNHASYII
16	1329.4	66.1	1758	8	BNHASYII
17	1326.6	66.0	1758	8	BNHASYII
18	1326.2	66.0	1758	8	BNHASYII
19	1316	65.5	1758	8	BNHASYII
20	1108.2	55.1	2156	8	BNHASYII
21	1107	55.1	2156	8	BNHASYII
22	1107	55.1	2156	8	BNHASYII
23	1106.6	55.1	2156	8	BNHASYII
24	1106.6	55.1	2156	8	BNHASYII
25	1106.6	55.1	2156	8	BNHASYII
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ALIGNMENTS

RESULT 1	AR148434	2365 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR148434	Sequence 1 from patent US 6225105.			
DEFINITION	Sequence 1 from patent US 6225105.				
ACCESSION	AR148434				
VERSION	AR148434.1	GI:15112524			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 2365)				
TITLE	Sathasivan, K. and Murai, N.				
JOURNAL	Mutant acetolactate synthase gene from Arabidopsis thaliana for conferring imidazolinone resistance to crop plants Patent: US 6225105-A 1 01-MAY-2001;				

FEATURES		Location/Qualifiers	
source	1..2365		
BASE COUNT	628 a 524 c 541 g 672 t		
ORIGIN			
Query Match 100.0%; Score 2010; DB 6; Length 2365;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 2010; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGCGGGGCAACAAACAAACAAACATCTCTTCGATCTCTCTTCCACCAACCA	60
DB	309	ATGGCGGGGCAACAAACAAACAAACATCTCTTCGATCTCTCTTCCACCAACCA	368
QY	61	TCT	120
DB	369	TCT	428
QY	121	ATCCCAACAAATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	180
DB	429	ATCCCAACAAATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	488
QY	181	TCCATCTCGCGGTCTCAACAAACAAACAAATGTCAACCACTCTCTCTCTCT	240
DB	489	TCCATCTCGCGGTCTCAACAAACAAACAAATGTCAACCACTCTCTCTCTCT	548
QY	241	CTTACCAACCGGAAACATTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT	300
DB	549	CTTACCAACCGGAAACATTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT	608
QY	301	GATATCT	360
DB	609	GATATCT	668
QY	361	GGTGCATCAATGGGATTCACCAAGCTTTAAGAGCTCAAGGCTAGAAACGG	420
DB	669	GGTGCATCAATGGGATTCACCAAGCTTTAAGAGCTTTAAGAGCTTTAAG	728
QY	421	CTCTGCTCGAAGAGGTGATTCGACGACGAGGATGAGCTCGATCTCTCT	480
DB	729	CTCTGCTCGAAGAGGTGATTCGACGACGAGGATGAGCTCGATCTCTCT	788
QY	481	CAAGGTATCTGTATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	540
DB	789	CAAGGTATCTGTATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	848
QY	541	GATGCTGTGTAGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	600
DB	849	GATGCTGTGTAGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	908
QY	601	ATTGGTACAGATGGGTTTCAAGACTCTCGATTTGAGGTAAAGGTTGAGTA	660
DB	909	ATTGGTACAGATGGGTTTCAAGACTCTCGATTTGAGGTAAAGGTTGAGTA	968
QY	661	CATACTATCTGTGATGGATGTTGAGATATCTCTCTCTCTCTCTCTCTCT	720
DB	969	CATACTATCTGTGATGGATGTTGAGATATCTCTCTCTCTCTCTCTCTCT	1028
QY	721	TTAGCTATCT	780
DB	1029	TTAGCTATCT	1088
QY	781	CAGCTTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	840
DB	1089	CAGCTTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1148
QY	841	CTTAAACCT	900
DB	1149	CTTAAACCT	1208
QY	901	AAGCTGTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	960
DB	1209	AAGCTGTGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1268

QY	961	GTTGAGCTTACGGGGATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1020
DB	1269	GTTGAGCTTACGGGGATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1328
QY	1021	GATGATGATGTTGCTTACATATGCTTGGGAATGATGGGATCTGTATGCA	1080
DB	1329	GATGATGATGTTGCTTACATATGCTTGGGAATGATGGGATCTGTATGCA	1388
QY	1081	GTTGGAGCATAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1140
DB	1389	GTTGGAGCATAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1448
QY	1141	AAGCTTGAAGCTTTTCTAGTAGGCTTAAGATGTTTATATGATTTAGCT	1200
DB	1449	AAGCTTGAAGCTTTTCTAGTAGGCTTAAGATGTTTATATGATTTAGCT	1508
QY	1201	ATTGGGAGATTAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1260
DB	1509	ATTGGGAGATTAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1568
QY	1261	GGGATGAATGAAGTTTCTGAGAACCGAGCGGAGGCTTAAAGCTTTGAG	1320
DB	1569	GGGATGAATGAAGTTTCTGAGAACCGAGCGGAGGCTTAAAGCTTTGAG	1628
QY	1321	AGGATGATGTTGAACCTTACGAAACAGAGCTTTCCGTTGAGCTTTAAG	1380
DB	1629	AGGATGATGTTGAACCTTACGAAACAGAGCTTTCCGTTGAGCTTTAAG	1688
QY	1381	GCTATCT	1440
DB	1689	GCTATCT	1748
QY	1441	ATAAGTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1500
DB	1749	ATAAGTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1808
QY	1501	CAAGCGAGTGGCTTATCATCAGAGGCTTTGAGGCTATGAGGATTTGAG	1560
DB	1809	CAAGCGAGTGGCTTATCATCAGAGGCTTTGAGGCTATGAGGATTTGAG	1868
QY	1561	ATTGGAGGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1620
DB	1869	ATTGGAGGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1928
QY	1621	TTTATATGATGTTGCAAGAGCTTACCACTATTTCTGTAGAGATCTTCC	1680
DB	1929	TTTATATGATGTTGCAAGAGCTTACCACTATTTCTGTGTAGAGATCTT	1988
QY	1681	CTTTTATATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1740
DB	1989	CTTTTATATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2048
QY	1741	GTTAAACCGAGCTTACCACTTTCTGCGGATCCGCTCTCAGGAGGAGAT	1800
DB	2049	GTTAAACCGAGCTTACCACTTTCTGCGGATCCGCTCTCAGGAGGAGAT	2108
QY	1801	ATGTTGCTGTTTTCAGCAGCTTTGCGGATTTCCAGCGCGGAGGTTGCA	1860
DB	2109	ATGTTGCTGTTTTCAGCAGCTTTGCGGATTTCCAGCGCGGAGGTTGCA	2168
QY	1861	CTCCGAGGAGCTTTCAGCAATGCTGTAACACGAGGCTTCTCTCTGTTG	1920
DB	2169	CTCCGAGGAGCTTTCAGCAATGCTGTAACACGAGGCTTCTCTCTGTTG	2228
QY	1921	TGTCGCGACCAAGAAATGTTGTTGCGGATGATCCGAATGTTGGGCTTC	1980
DB	2229	TGTCGCGACCAAGAAATGTTGTTGCGGATGATCCGAATGTTGGGCTTC	2288
QY	1981	ATAACGAGGAGGATGCGCGGATTAATATAC	2010
DB	2289	ATAACGAGGAGGATGCGCGGATTAATATAC	2318







Db	38677	CTCGCTCAACGAACGAGGCTGTTATTCGCGACGAGAGGATA CGCTCGATCTCAGGTAAA	386118
Qy	481	CCAGGTATCTGTATAGCCATCTCAGGTCCTCCGAGCTCAAACTCTGTTAGCGGATTA GCC	540
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Qy	541	GATCGCTCTGTATAGTATGTTCTCTTGTAGCAATCA CAGGCAAGTCCTCGTCGTATG	600
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Qy	661	CATAA CTATCTGTGATGAGATGTTGAAGATATCCCTAGGATTA TTAGGAGCTTCTTT	720
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Qy	721	TTAGCTATCTTCTGTAGACCTGTGACCTGTTTGTGATGTTTCTTAAGATATTCACAA	780
Db	38377	TTAGCTATCTTCTGTAGACCTGTGACCTGTTTGTGATGTTTCTTAAGATATTCACAA	38318
Qy	781	CAGCTTGCATCTCTTAATTTGGGAACAGGCTATGAGATTACCTGGTTATATGTTAGATG	840
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Qy	841	CTTAAACCTCCGGAAGATTCATATTTGGAGCAGATGTTTAGTTGATTTCTGAGTCTAAG	900
Db	38257	CTTAAACCTCCGGAAGATTCATATTTGGAGCAGATGTTTAGTTGATTTCTGAGTCTAAG	38198
Qy	901	AAGCTGTCTGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	960
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Qy	1021	GATGATGATCTGTCTTACATATGTTTGGAGTATGTTGATGATGATGATGATGATGATG	1080
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Qy	1081	GTGGAGCATAGTGAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1140
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Qy	1141	AAGCTTGAAGCTTTTCTAGTGGCTTAAGATGTTTCAATTTGATTTGATTTGATTTGAT	1200
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Qy	1201	ATTGGGAAGATTAAGACTCTCTCATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1260
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Qy	1261	GGATGATTAAGCTTTCTTGAACCCGAGCGAGGCTTAAGCTTGAATTTGAGATTTGG	1320
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Qy	1321	AGGATGATTTGAAGCTTACAGAAACAGAGTTTCCGTTGAGCTTTTAAGACGTTTGGGAA	1380
Db	37777	AGGATGATTTGAAGCTTACAGAAACAGAGTTTCCGTTGAGCTTTTAAGACGTTTGGGAA	37718
Qy	1391	GCTATTCCTCCACATATGCGATTAAGCTTCTTGAATGTTGATGTTGATGTTGATGTTG	1440
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Qy	1441	ATAAGTACTGTTGCTGCGACACATCAAAATGCGGCGGCGAGTCTTCAATTAACAGAA	1500
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Qy	1501	CCAAGGCACTGCTATCATCAGGAGGCTTTGAGATGTTGGATTTGCACTTCTGCTGG	1560
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Qy	1561	ATTGAGCGCTCTGTTGCTAACCTCATCCGATAGTGTGATGATGATGATGATGATGATG	1620
Db	37537	ATTGAGCGCTCTGTTGCTAACCTCATCCGATAGTGTGATGATGATGATGATGATGATG	37478
Qy	1621	TTTATAATGAATGTCAGAGAGCTAGCCATTTCTGTTAGAGAAATCTTCCAGTGAAGTA	1680
Db	37477	TTTATAATGAATGTCAGAGAGCTAGCCATTTCTGTTAGAGAAATCTTCCAGTGAAGTA	37418
Qy	1681	CTTTTATTAACACACAGCATCTTGGCATGTTATGCAATGGAGATGCGTTCACAAA	1740
Db	37417	CTTTTATTAACACACAGCATCTTGGCATGTTATGCAATGGAGATGCGTTCACAAA	37358
Qy	1741	GCTAACCCGAGCTCACACATTTCTCGGGATCCCGGCTCAGAGGACGACATATCCCGAAC	1800
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Qy	1801	ATGTTGCTGTTTTCAGAGCTTTCGGGATTCAGAGCGCGAGGGTGA CAAAGAAAGCAT	1860
Db	37297	ATGTTGCTGTTTTCAGAGCTTTCGGGATTCAGAGCGCGAGGGTGA CAAAGAAAGCAT	37238
Qy	1861	CTCCGAGAGCTATTACAGCAATGCTGATACACAGGACCTTA CTTGTTGGATGTTGAT	1920
Db	37237	CTCCGAGAGCTATTACAGCAATGCTGATACACAGGACCTTA CTTGTTGGATGTTGAT	37178
Qy	1921	TGTCGCGACCAAGAAATGTTGCTGATGATGATGATGATGATGATGATGATGATGATG	1980
Db	37177	TGTCGCGACCAAGAAATGTTGCTGATGATGATGATGATGATGATGATGATGATGATG	37118
Qy	1981	ATAACGAGAGGAGATGCGCGATTAATAATAC	2010
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DEFINITION	Arabidopsis thaliana acetolactate synthase (T8P19.70) mRNA,		
complete cds.			
ACCESSION	AY042819	GI:14596062	
VERSION	AY042819.1		
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana.		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			

e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PCEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs : Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

Submitted (25-JUN-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA



Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs.

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		PGICITSGGATNVLAVGASLADLDSVPLVITGVQPRMIGTDAFQETPIVEVTSRI	
		TKNYLVMQVEDIPRIIEEAFATISGRPGPVLVDVPRKDIQOOLAIINWEQAMRLPGY	
		MSRKPDPDELHLEQIVRLISSEKPVLYVGGCLNSSLDELGRVELTIGIPVASTMG	
		LGSVPDDELSLHLMGHGTGVYANYAVERSDLLAFGVRFDRVTGKLKAFASRAKIV	
		HIDDSAEIKNKTPEHVSQGVKALQGNKVLNRAELKLDGVWNLNLOKQK	
		PPLSKFTGPAIPPOYAIVKLDLTDGKALISTGVGQHMWAQFVNYKKPQLWSSG	
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Query Match		99.88;	Score 2005.2; DB 8; Length 2263;
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Matches 2007;		Conservative 0;	Mismatches 3; Indels 0; Gaps 0;
QY	1	ATGGCGGGGCAACAAACAAACAAACATCTTCTTCGATCTCTCTCCATCCCAACCA	60
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QY	181	TCT	240
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QY	301	GATATCT	360
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QY	541	GATCGTGTGTAGATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	600
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Db	640	ATTGTGACAGATCGGTTTCAAGAGATCTCCGATTTGTGAGTTAAACCGTTGATTA	699
QY	661	CATAACTATCTCTGTATGATCTGAGATATCCCTAGGATTTATGAGGAGCTTTCTT	720
Db	700	CATAACTATCTCTGTATGATCTGAGATATCCCTAGGATTTATGAGGAGCTTTCTT	759
QY	721	TTAGCTACTTCTGTAGACCTGACCTGTTTGTGTTGATGTTCTTAAAGATATTCAACA	780
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QY	781	CAGCTTGGATCTCTAATTTGGGACACGCTATGAGTATACCTGTTATATGTTAGGAT	840
Db	820	CAGCTTGGATCTCTAATTTGGGACACGCTATGAGTATACCTGTTATATGTTAGGAT	879
QY	841	CTTAAACCTCCGGAAGATTTCTCATTTGGAGCAGATTTGTTAGGTTGATTTCTGAGT	900
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QY	901	AAGCCTGTGTGTATCTTGGTGGTGTGTTGTTGAAATTTCTAGCGATGATTTGGTGT	960
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QY	961	GTTGAGCTTACCGGGATCTCTCTGCGAGTACCTTGCATGGGGCTGGGATCTTATCTCT	1020
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QY	1021	GATGATGATGTTCTGTTA CATATGCTTGGATTCGATCGGACCTGCTATGCAATTAAGT	1080
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QY	1321	AGGAATGATGTTGAACCTTACAGAAACAGAGTTTCCCTGAGCTTTAAGCTTTGGGAA	1380
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QY	1441	ATPAGTACTGTTGTCCGGGACACATCAATGTGGGCGGCGAGTTCTCAATTAAGAA	1500
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QY	1501	CAAGGCAAGTGGCTTATCATCAGAGGCTTTGGAGCTATGAGGATTTGGACTTCTCTGCTGG	1560
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QY	1561	ATPAGGAGCTTCTGTCTTAAACCTTGATCGGATGTTGTTGATTAATTAAGCGGAGTGAAGC	1620
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RESULT 5  
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 ORGANISM Arabidopsis thaliana.  
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 1 (bases 1 to 2013)  
 Jander,G., Baerson,S.R., Hudak,J.A., Gonzalez,K.A., Gruys,K.J. and Last,R.L.  
 Saturation mutagenesis in Arabidopsis to determine frequency of herbicide resistance  
 Unpublished  
 2 (bases 1 to 2013)  
 Jander,G., Baerson,S.R., Hudak,J.A., Gonzalez,K.A., Gruys,K.J. and Last,R.L.  
 Direct Submission  
 Submitted (19-JUN-2002) Boyce Thompson Institute, Tower Road, Ithaca, NY 14850, USA  
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REFERENCE 1 (bases 1 to 3386)  
AUTHORS Rutledge, R.G., Quillet, T., Hattori, J., and Miki, B.L.  
TITLE Molecular characterization and genetic origin of the Brassica napus  
acetoaldehyde synthase multigene family  
JOURNAL Mol. Gen. Genet. 229 (1), 31-40 (1991)  
MEDLINE 91375448  
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REFERENCE 2 (bases 1 to 3386)  
AUTHORS Miki, B.